# course coese

Description  "potassium transport protein, high- affinity; potassium transport protein TRK1, high-affinity - yeast (Saccharomyces cerevisiae) (strain Saccharomyces uvarum); (M57508) high-affinity K+ transporter [Saccharomyces uvarum] "	(AB014569) KIAA0669 protein [Homo sapiens]	(D89340) dipeptidyl peptidase III [Rattus norvegicus]	hypothetical 54.1 KD protein in TPS3- IPP2 intergenic region; hypothetical protein YMR265c - yeast (Saccharomyces cerevisiae); (Z49260) unknown [Saccharomyces cerevisiae]	(AF052606) chitin synthase 2 [Exophiala dermatitidis]	hypothetical 65.9 KD protein C31A2.12 in chromosome I; hypothetical protein SPAC31A2.12 - fission yeast (Schizosaccharomyces pombe); (Z50113) unknown [Schizosaccharomyces pombe]	(U78318) chitinase [Entamoeba dispar]	(AE000888) malate dehydrogenase [Methanobacterium thermoautotrophicum]	(AL022598) hypothetical protein [Schizosaccharomyces pombe]	(AF009921) I100 [Rattus norvegicus]	enoyl-[acyl-carrier-protein] reductase (NADH) (NADH-dependent enoyl-ACP reductase)	(AJ011965) oxidoreductase [Claviceps purpurea]
% cvrg		18	27	17			69	25	37		24
Blast Prob % id 4.00E-32 38	2.7	5.00E-11 35	0.000000 32 03	1.00E-29 40	0.0007	6.00E-22	2.00E-41 38	9.00E-13 26	2.00E-42 37	0.000000	0.000001 37
Blast Score 138	32	89	54	129	45	48	169	75	172	59	54
aat Score 283	62	78	70	270	479	221	390	254	572	77	134
ncbi gi g136230	g3327152	g2832906	g2497213	g3548904	g1175406 479	g1685360	g2622314	g3080513	g2653779	g1169593	g4499843
Database Hit											
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 738-757	458-479	481-504	450-477	375-398	761-780	792-811	578-597	805-829	723-749	454-479	582-601
Primer 5 pos 25-45	108-134	55-74	22-46	27-46	25-44	53-72	23-42	22-49	92-111	36-63	52-71
Seq num Seq id Contig source 5 23214 ENU07008 ANI61C6898: 2 2691113	23215 ENU07009 ANI61C9885: 108-134 458-479 16091943	23216 ENU07010 ANI61C89:88 55-74 71411	23217 ENU07011 ANI61C137:2 22-46 4842939	23218 ENU07012 ANI61C9887: 27-46 45364956	23219 ENU07013 ANI61C9344: 25-44 11833128	23220 ENU07014 ANI61C6320: 53-72 26541308	<del>)</del> 6:	23222 ENU07016 ANI61C2287: 22-49 58294008	23223 ENU07017 ANI61C1403: 92-111 15121	23224 ENU07018 ANI61C8897: 36-63 1180874	23225 ENU07019 ANI61C9319: 52-71 79758612

#### catto cato

Description (AL021813) hypothetical protein [Schizosaccharomyces pombe]	(Z98603) hypothetical protein [Schizosaccharomyces pombe]	"protein phosphatase 2C (PP2C); phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramecium tetraurelia (SGCS); (Z36985) PP2C [Paramecium tetraurelia]"	(AF091042) putative cercosporin transporter [Cercospora kikuchii]	cytochrome C oxidase assembly protein COX10 precursor; COX10 protein precursor - yeast (Saccharomyces cerevisiae); (M55566) COX10	[Saccharomyces cerevisiae]; (Z73528) ORF YPL172c [Saccharomyces cerevisiae]	(AB004535) hypothetical protein YPR112c [Schizosaccharomyces pombe]	(U68040) polyketide synthase [Cochliobolus heterostrophus]	nitrogen assimilation transcription factor NIRA; nitrate assimilation regulatory protein nirA - Emericella nidulans; (M68900) NIRA protein [Emericella nidulans]	(AB014471) compaired with Cricetulus griseus SL15 mRNA; GenBank Accession Number U55387 [Mus musculus]	SPO14 protein - yeast (Saccharomyces cerevisiae); (Z28256) ORF YKR031c [Saccharomyces cerevisiae]	(L19875) Dur3 [Saccharomyces cerevisiae]
% id cvrg	33		42	57			Ξ		58	12	38
% id	38		28	47			29		1 34	3 43	7 40
Blast Prob 0.0002	6.00E-28 38	0.00000	5.00E-20 28	4.00E-60 47		0.0002	2.00E-28 29	0.0003	4.00E-14 34	5.00E-38 43	7.00E-57 40
Blast Score 46	123	51	82	137		46	126	46	78	121	220
aat Score 87	275	42	208	584		577	735	158	151	840	1750
ncbi gi g2879805	g2330876	g1352686	g3885836	g117135		g2257512	g1546072	g128340	g3165391	g539247	g388367
Database Hit ncbi gi g28798											
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 446-465	497-521	411-430	805-829	789-807		783-802	810-829	765-784	405-425	802-829	805-829
Primer 5 pos 55-75	22-43	27-49	65-84	22-42		35-54	29-49	28-48	22-49	22-42	23-42
Seq num Seq id Contig source 23226 ENU07020 ANI61C1431: 13071908	17:	370: 6	23229 ENU07023 ANI61C2346: 65-84 11323	23230 ENU07024 ANI61C1412: 22-42 26651680		23231 ENU07025 ANI61C6288: 35-54 21421088	23232 ENU07026 ANI61C6888: 29-49 12334	23233 ENU07027 ANI61C8905: 28-48 19381	23234 ENU07028 ANI61C1412: 22-49 34413876	23235 ENU07029 ANI61C8909: 22-42 5301462	23236 ENU07030 ANI61C6288: 23-42 69784884

# countain compos

	granaticin polyketide synthase putative ketoacyl reductase 1 (ORF5); granaticin-producing polyketide synthase chain 5 - Streptomyces violaceoruber; (X16144) ketoacyl reductase (AA 1-273) [Streptomyces violaceoruber]; (X16300) ORF 5 (AA 1-272) [Streptomyces violaceoruber]; (X16300) ORF 5 (AA 1-272) [Streptomyces violaceoruber]; (AJ011500) polyketide ketoreductase	[Streptomyces violaceoruber] modifier 3 protein (M33); modifier-3 protein - mouse; (X62537) modifier 3	(AF060544) androgen receptor	associated protein 34 (nomo saprens) (AL031518) putative phosphpolipase (Schizosocharomyzes nombe)	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae); (U10400)	r sco4p [saccharomyces cerevisiae] (AL031856) hypothetical protein	[Schizosaccharomyces pombe] KI3 protein; probable membrane protein YLR384c - yeast (Saccharomyces cerevisiae); (U19104) Ki3p [Saccharomyces cerevisiae]; (D87841) Ki3p [Saccharomyces	ubiquitin carboxyl-terminal hydrolase 16 (ubiquitin thiolesterase 16) (ubiquitin-specific processing protease 16) (deubiquitinating enzyme 16); probable membrane protein YPL072w - yeast (Saccharomyces cerevisiae); (U41849) Lpf12p [Saccharomyces
% id cvrg			30	35	42	34	7	28
	9		29	1 37	9 40	3 34	3 49	27
Blast Prob 7.00E-10	6.00E-26	5.3	0.08	3.00E-31	4.00E-19 40	5.00E-23 34	4.00E-13 49	0.00002
Blast Score 65	118	31	37	135	75	85	47	50
aat Score 85	164	86	73	372	199	310	219	119
ncbi gi g122798	g118571	g266545	g4530066 73	g3560189	g626598	g3738165 310	g2498477 219	g3334399
Database Hit ncbi gi g12275								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 772-792	716-735	520-539	. 459-478	723-749		789-815		744-764
Primer 5 pos 22-47	26-53	24-43	102-124	24-48		22-48		111-131
Seq Prime num Seq id Contig source 5 pos 23237 ENU07031 ANI61C8926: 22-47	23238 ENU07032 ANI61C1439: 26-53 6501414	23239 ENU07033 ANI61C8916: 24-43 282845	23240 ENU07034 ANI61C3321: 102-124 459-478	5101 23241 ENU07035 ANI61C9931: 24-48	23242 ENU07036 ANI61C322:6 921337	23243 ENU07037 ANI61C6894: 22-48	1533.2570 23244 ENU07038 ANIGIC2329: 54875174	23245 ENU07039 ANI61C6906: 111-131 744-764 1797
Seq num 23237	23238	23239	23240	23241	23242	23243	23244	23245

# certain serio

	guanosine-diphosphatase (GDPASE); guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae); (L19560) guanosine diphosphatase [Saccharomyces cerevisiae]; (U18779) Gda1 p: guanosine-diphosphatase of Golgi membrane [Saccharomyces	(U78320) chitinase [Entamoeba invadens]	(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]	membrane transporter DI; membrane transport protein (clone DI.SH) - Leishmania donovani; (M85072) DI transporter [Leishmania donovani]; myo-inositol/H symporter [Leishmania donovani]	(AL021046) positive regulator of camp dependent protein kin ase	(AC006067) hypothetical protein [Arabidopsis thaliana]	(AF015775) acetylomitine deacetylase [Bacillus subtilis]; (Z99114) acetylomitine deacetylase [Bacillus subtilis]	FAB1 protein - yeast (Saccharomyces cerevisiae); (D50617) FAB1 protein [Saccharomyces cerevisiae]	YFW1 gene [Saccharomyces cerevisiae]
%	% 1d cvrg 55 29	45	19		19	16	20	12	29
	% 10 3 55 10 10 10 10 10 10 10 10 10 10 10 10 10	30	98		3 34	5 42	3 32	9 39	1 32
	Prob % 1.00E-38 55	1.00E-29 30	e-144	0.00007	3.00E-18 34	3.00E-35 42	1.00E-23 32	1.00E-59 39	8.00E-11 32
Blast	Score 159	130	510	47	92	86	109	230	<i>L</i> 9
aat	335 335	233	1664	43	157	350	232	546	126
	ncbi gi g418404	g1685364	g3282044 1664	g544446	g2706465 157	g4263825	g2415403	g1084543	g1582765 126
	Database Hit								
Selection	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 455-479	576-595	725-749	410-430		567-586	566-588	805-823	488-507
Primer	22-41	22-47	29-48	53-71		38-59	23-42	88-69	27-54
	Contig source ANI61C9403: 13441768	ANI61C3333: 34334136	ANI61C2366: 11501	ANI61C691:8 84564	ANI61C9381: 34563877	ANI61C2373: 815203	ANT61C1454: 6681	ANI61C6226: 2377306	ANI61C992:7 691308
	num Seq id Contig source 5 pos 23246 ENU07040 ANI61C9403: 22-41 13441768	23247 ENU07041 ANI61C3333: 22-47 34334136	23248 ENU07042 ANI61C2366: 29-48 11501	23249 ENU07043 ANI61C691:8 53-71 84564	23250 ENU07044 ANI61C9381: 34563877	23251 ENU07045 ANI61C2373: 38-59 815203	23252 ENU07046 ANI61C1454: 23-42 6681	23253 ENU07047 ANI61C6226: 69-88 2377306	23254 ENU07048 ANI61C992:7 27-54 691308

# Corcess cesses

Description meiosis induction protein kinase IME2/SME1; probable protein kinase SME1 (EC 2.7.1) - yeast (Saccharomyces cerevisiae); (X53262) protein kinase homologue [Saccharomyces cerevisiae]; (X49381) ORF YIL106w [Saccharomyces cerevisiae];	(AL023592) ma binding protein [Schizosaccharomyces pombe]	(Y12709) tealp [Schizosaccharomyces pombe]; (AL031579) cell polarity protein [Schizosaccharomyces pombe]	hypothetical 98.4 KD protein C19G10.07 in chromosome I; (Z69909) multiple BRCT domain containing protein [Schizosaccharomyces pombe]	hypothetical 130.0 KD protein in SNF6-SPO11 intergenic region; hypothetical protein YHL023c - yeast (Saccharomyces cerevisiae); (U11582) No definition line found (Saccharomyces cerevisiae)	hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae); (Z74957) ORF YOR049c [Saccharomyces cerevisiae]	histone H1.1; histone H1.1 - Arabidopsis thaliana; (X62458) Histone H1 [Arabidopsis thaliana]	transaldolase ; (L47327) transaldolase [Anabaena variabilis]	(Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
% id cvrg 35 29	21	21	29		89		45	<b>∞</b>
% id	4 26	8 38	7 28	7	7 33		0 33	8 31
Blast Prob % i 3.00E-11 35	2.00E-24 26	3.00E-48 38	4.00E-27 28	3.00E-17	5.00E-17 33	1.2	5.00E-10 33	2.00E-28 31
Blast Score 50	113	192	122	71	78	33	42	126
aat Score 145	282	609	322	169	215	98	114	412
ncbi gi g417780	g3136059	g2065436	g1723501	g731604	g2132036	g121902	g1729831	g2440180 412
Database Hit ncbi gi g41778								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos	784-803	803-829	717-741	804-824	805-826	452-479	374-392	806-829
Primer 5 pos	23-43	28-55	22-42	121-140	22-41	102-124	22-41	72-91
Seq   1   23255 ENU07049 ANI61C2379: 8351525	23256 ENU07050 ANI61C6348: 23-43 10901	23257 ENU07051 ANI61C6908: 28-55 1934721	23258 ENU07052 ANI61C9404: 22-42 12861	23259 ENU07053 ANI61C9946: 121-140 804-824 11277	23260 ENU07054 ANI61C1405: 22-41 52706129	23261 ENU07055 ANI61C6251: 102-124 452-479 3581	23262 ENU07056 ANI61C6955: 22-41 5401014	23263 ENU07057 ANI61C9408: 72-91 25591452
Seq. num 23255	2325(	2325	2325	2325	2326	2326	2326.	2326.

# oceeo. Cennon

	proteins [Saccharomyces cerevisiae] hypothetical 37.9 KD protein in STE12-NAM8 intergenic region; hypothetical protein YHR085w - yeast (Saccharomyces cerevisiae); (U10556)	STB2 protein; SIN3 protein-binding protein STB2 - yeast (Saccharomyces cerevisiae); (Z49703) unknown [Saccharomyces cerevisiae]; (U33438) Stb2n [Saccharomyces cerevisiae]	(AL03551) hypothetical protein (Arabidonsis thaliana)	(AL034352) hypothetical protein [Schizosaccharomyces pombe]	(Z98849) putative dna repair helicase [Schizosaccharomyces pombe]	hypothetical 71.9 KD protein in PMI40-PAC2 intergenic region; hypothetical protein YER005w - yeast (Saccharomyces cerevisiae); (U18778) Yer005wp [Saccharomyces cerevisiae]	(Z98849) putative centromere protein [Schizosaccharomyces pombe]	(AB004539) hypothetical 229.9KD protein in NUC1-PRP21 intergenic region [Schizosaccharomyces pombe]	(AL034353) probable metabolite transport protein [Schizosaccharomyces pombe]
%   cvrg   9	49	33	26	51	34	22	25	11	46
% id	) 26	30	3 36	36	74	1 36	1 35	3 30	9 43
Blast Prob % 1.00E-20 43	0.000000 26	5.00E-28 30	1.00E-38 36	0.000000 36	e-106	3.00E-21 36	2.00E-24 35	1.00E-18 30	2.00E-29 43
Blast Score 99	56	125	160	48	354	74	111	93	78
aat Score 181	143	258	478	229	1370	216	227	173	835
ncbi gi g730745	g731682	g1711559	g4455171	g3925763	g2370478 1370	g731435	g2370479	g2257560	g3925778
n Database Hit									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 299-321	391-417	786-805	806-828	416-435	801-821	416-435	457-479	579-606	805-824
Primer 5 pos 107-127	104-130	58-77	22-49	28-69	39-66	134-157	98-59	33-52	22-44
Primer Primer Seq id Contig source 5 pos 3 pos ENU07058 ANI61C3372: 107-127 299-321 1343	23265 ENU07059 ANI61C2389: 104-130 391-417 4361	23266 ENU07060 ANI61C1400: 58-77 77908761	23267 ENU07061 ANI61C3370: 22-49	23268 ENU07062 ANI61C1472: 69-87 20441716	23269 ENU07063 ANI61C6341: 39-66 18052935	23270 ENU07064 ANI61C6930: 134-157 416-435 49244444	23271 ENU07065 ANI61C9421: 65-86 3901	23272 ENU07066 ANIGIC1483: 33-52 850202	23273 ENU07067 ANI61C6334: 22-44 8832416
Seq num 23264	23265	23266	23267	23268	23269	23270	23271	23272	23273

# common compo

Description SMM1 protein; hypothetical protein YNR015w - yeast (Saccharomyces cerevisiae); (Z71630) ORF YNR015w [Saccharomyces cerevisiae]; (X91816) SMM1 protein [Saccharomyces	cutinase transcription factor 1 beta; (U51672) cutinase transcription factor	I [Fusarium solani T. sp. pisi] (AB015724) nuclear receptor binding factor-I [Rattus norvegicus] (Z98603) putative proteosome	component [Schizosaccharomyces pombe] (AJ011965) oxidoreductase [Claviceps	purpureaj (AB010110) ascorbate oxidase [Acremonium sp.]	(Z99113) polyketide synthase [Bacillus subtilis]	chromosome 22 open reading frame 1; (U84894) 239AB [Homo sapiens]	(AE000990) aspartate aminotransferase (aspB-3) [Archaeoglobus fulgidus]	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]	Cation-transporting ATPase PAT1; PAT1 protein - slime mold (Dictyostelium discoideum); (X89369) PAT1 protein [Dictyostelium discoideum]	(AC004682) pre-mRNA splicing factor (PRP16)(KIAA0224) [Homo sapiens]	"carboxypeptidase S1; carboxypeptidase S1 - Penicillium janthinellum; carboxypeptidase S1, CPD-S1 [Penicillium janthinellum, Peptide, 423 aa]; carboxypeptidase S1 [Penicillium janthinellum]"
% cvrg	27	33	25	34	4	61		16	24	23	33
% id 4 40	5 43	1 45	42	1 52	31	2 33	0	7 32	7 48	29	2 39
Blast Prob % 1.00E-44 40	1.00E-45 43	2.00E-21 45 5.00E-60 58	0.0002	2.00E-51 52	2.00E-20	1.00E-22 33	0.000000	7.00E-27 32	4.00E-47 48	e-105	8.00E-22 39
Blast Score 152	183	101	45	202	66	106	38	121	188	380	104
aat Score 698		193 656	204	467	208	158	102	570	758	1305	575
ncbi gi g1730664	g1706177 1207	g3970880 g2330868	g4499843	g2780359	g2634103	g4502497	g2648929	g3650387	g1703456	g3337389 1305	g461830
Database Hit											
Selection Basis LINAP	LINAP	LINAP LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 803-829	802-829	349-368	312-330	573-597	525-544	522-541	800-819	805-829	772-791	761-780	808-829
Primer 5 pos 22-46	22-44	102-124	34-53	28-47	54-78	106-133	22-44	36-55	22-46	22-44	22-41
Contig source ANI61C6965: 5081471	ANI61C9916: 3241953	ANI61C1467: 1392 ANI61C6366:	43918 ANI61C6991:		ANI61C237:1 8222409	ANI61C9452: 1566	ANI61C6338: 24201309		ANI61C3374: 22-46 10982512	ANI61C7547: 13061	ANI61C9916: 40115218
Seq num Seq id 23274 ENU07068	23275 ENU07069 ANI61C9916: 22-44 3241953	23276 ENU07070 ANI61C1467: 102-124 349-368 1392 23277 ENU07071 ANI61C6366: 41-63 790-811	43918 23278 ENU07072 ANI61C6991: 34-53	23279 ENU07073	23280 ENU07074 ANI61C237:1 8222409	23281 ENU07075 ANI61C9452: 106-133 522-541 1566	23282 ENU07076 ANI61C6338: 22-44 24201309	23283 ENU07077	23284 ENU07078	23285 ENU07079 ANI61C7547: 22-44 13061	23286 ENU07080 ANI61C9916: 22-41 40115218

	(U63409) Slazp [ Y аггоміа проіуцса]	(AL03452) putative phophodiesterase-nucleotide pyrophosp hatase precursor [Schizosaccharomyces pombe]	putative kinesin-like protein C2F12.13; (Z97211) kinesin-like protein [Schizosaccharomyces pombe]	hypothetical 39.7 KD protein in HOM6-PMT4 intergenic region; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae); (Z49642) ORF YJR142w [Saccharomyces cerevisiae]	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus] "	probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae); (U19027) Ylr222cp [Saccharomyces cerevisiae]	hypothetical protein YDR456w - yeast (Saccharomyces cerevisiae); (U33007) Ydr456wp; CAI: 0.16 [Saccharomyces cerevisiae]	(U97681) putative splicing factor [Schizosaccharomyces pombe]; (AL035675) putative splicing factor. [Schizosaccharomyces pombe]	(Z98529) mating and morphogenesis protein Scd1p. [Schizosaccharomyces pombe]
	51	30	32	09	83		27	56	
% id 24	S	40	5 54	37	2 50		7 40	3 47	~
	7.00E-30 55	1.00E-22 40	7.00E-66 54	9.00E-29 37	4.00E-42 50	0.0007	1.00E-22 40	3.00E-33 47	4.00E-23
	\$	106	250	127	171	4	106	06	88
aat Score 99	312	225	762	294	334	114	282	478	240
ncbi gi g3319757	g39/8134	g3925755	g3219911	g1352938	g2648302	g1077378 114	g2131504	g2911284	g2330697 240
Database Hit ncbi gi									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 808-827	456-483	372-399		554-579	693-715	465-492		803-822	796-815
Primer 5 pos 22-44	22-46	22-44		44-63	23-48	22-48		53-72	40-60
Seq Prime  13287 ENU07081 ANI61C3345: 22-44  1879983	23288 ENU07082 ANI61C6996: 22-46 5381118	23289 ENU07083 ANI61C3379: 22-44 17622136	23290 ENU07084 ANI61C239:1 917	23291 ENU07085 ANI61C6990: 44-63 6291	23292 ENU07086 ANI61C7552: 23-48 1664929	23293 ENU07087 ANI61C9970: 22-48 412945	23294 ENU07088 ANI61C3355: 1522	23295 ENU07089 ANI61C2400: 53-72 1911895	23296 ENU07090 ANI61C6338: 40-60 67865567
Seq num Seq id 23287 ENUO	23288 EN	23289 ENI	23290 ENI	23291 ENI	23292 ENI	23293 EN	23294 EN	23295 EN	23296 EN

# Cotoucad cesoo

	Description putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme); (Z54096) unknown	[SCIIIZOSACCIAIOIII] (Z97341) heat shock protein 110 homolog [Arabidonsis thaliana]	phosphate transporter - Glomus versiforme ; (U38650) phosphate	transporter [Glomus versiforme]; phosphate transporter [Glomus versiforme]	(U14651) protein VI precursor [Human adenovirus type 40]	(AF041050) 4-coumarate: CoA ligase	probable membrane protein YOL146w	<ul> <li>yeast (Saccharomyces cerevisiae);</li> <li>(Z48239) orf6 [Saccharomyces cerevisiae];</li> <li>(Z74888) ORF YOL146w</li> </ul>	[Saccharomyces cerevisiae] (Z68906) ATP-binding multidrug cassette transporter [Botrvotinia	fuckeliana] (AL021646) hypothetical protein Rv3161c [Mycobacterium tuberculosis]	"multidrug resistance protein, canalicular - human; (X96395)	canalicular multidrug resistance protein [Homo sapiens] " (AF032987) spindle assembly checkpoint protein SLDA [Emericella nidulans]
%	cvrg 33	57	47				52		6	54	10	23
	% id 35	30	40				40		34	30	30	96
Blast	Prob 3.00E-21	3.00E-15	2.00E-30 40		0.29	1.00E-11	0.00006		2.00E-12	4.00E-10 30	0.000000 30 01	e-135
Blast	Score 67	82	132		36	71	48		46	63	4	415
aat	Score 210	125	609		72	82	93		131	149	61	5014
	g1174862	g2245021	g2147899		g725498	g3258637	g2132853		g3114719	g2827571	g2135769	g3136094 5014
	Database Hit											
Selection	Basis LINAP	LINAP	LINAP		LINAP	LINAP	LINAP		LINAP	LINAP	LINAP	LINAP
Primer	382-404	287-306	807-829		519-538	556-575	384-403		434-453	602-623		
Primer	5 pos 27-45	22-49	22-49		99-85	29-78	163-182		98-99	22-49		
	Contig source ANI61C1504: 5081	23298 ENU07092 ANI61C6368: 22-49			23300 ENU07094 ANI61C6335: 66-85 3430.4017	23301 ENU07095 ANI61C7006: 59-78	23302 ENU07096 ANI61C6335: 163-182 384-403	75998160	23303 ENU07097 ANI61C7575: 66-86 4191	23304 ENU07098 ANI61C9442: 22-49 41913548	23305 ENU07099 ANI61C3385: 11261478	23306 ENU07100 ANI61C2418: 13138
Seq	num Seq id 23297 ENU07091	23298 ENU07	23299 ENU07093		23300 ENU070	23301 ENU070	23302 ENU07		23303 ENU07	23304 ENU070	23305 ENU07	23306 ENU07

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Description (Z49908) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk434d4.5 comes from this gene; cDNA EST.; (Z81573) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk43d4.5 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA EST EMBL:D27475 comes	probable membrane protein YPR157w probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae); (U28371) P9584.4 gene product	loaccharonnyces cerevisiae, neutrophil cytosolic factor 2; p67phox; 67K neutrophil oxidase factor - human ; (M32011) neutrophil oxidase factor	elongation factor 1-gamma (EF-1-gamma); translation elongation factor eEF-1 gamma chain - brine shrimp; (M28020) elongation factor 1-gamma	[Artemia sp.] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
% id cvrg	30	35	17	29
	29 48	19 31	900 44	13 24
Blast Prob 0.000000 04	3.00E-29 48	3.00E-19 31	0.000000 44	9.00E-13 24
Blast Score 57	113	74	54	75
aat Score 126	345	172	149	110
ncbi gi g3874095	g2133035	g4557787	g119164	g2462679 110
Database Hit				
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 339-363	457-479	550-572	457-479	785-809
Primer 5 pos 102-127	45-72	68-94	22-48	22-42
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 23307 ENU07101 ANI61C1519: 102-127 339-363 1384	23308 ENU07102 ANI61C6992: 45-72 4121	23309 ENU07103 ANI61C7532: 68-94 1595	23310 ENU07104 ANI61C9963: 22-48 920596	23311 ENU07105 ANI61C3351: 22-42 61147195
Seq id ENU07101	: ENU07102	ENU07103	) ENU07104	ENU07105
Seq num 23307	23308	23309	23310	23311

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	(AL023860) hypothetical protein [Schizosaccharomyces pombe]	(AC002342) putative Cu2+- transporting ATPase [Arabidopsis thaliana]	UFE1 protein; UFE1 protein - yeast (Saccharomyces cerevisiae); (L.15081) UFE1 gene product [Saccharomyces cerevisiae]; (U53416) Ufe1p	ORF YOR075w [Saccharomyces cerevisiae]; (Z70678) YOR29-26 [Saccharomyces cerevisiae]	myo-inositol transporter 1; (X98622) myo-inositol transporter (Schizosaccharomyces nombel	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus	(U58946) transposase [Aspergillus awamori]	(Z98981) hypothetical protein [Schizosaccharomyces pombe]	(AF035401) exocellobiohydrolase precursor [Piromyces rhizinflata]	(Z98885) dJ522J7.2 (Peregrin (BR140) like protein) [Homo sapiens]	(U16137) Mvp1p [Saccharomyces cerevisiae]	(AJ006340) 26S proteasome subunit p112 [Rattus norvegicus]	hypothetical protein C22F3.14C in chromosome I; hypothetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe); (Z54285) unknown [Schizosaccharomyces pombe]
	34	23	40		28		28				16	Ξ	∞
% id 5 38	38	, 30	23		44		5 32	C		~	39	8 44	t 36
	6.00E-24	1.00E-17 30	0.0001		2.00E-26 44	900.0	3.00E-16 32	0.000000	0.11	3.00E-13	0.000000 39 002	3.00E-18 44	1.005-14 36
	111	06	46		74	41	85	61	38	9/	62	74	08
aat Score 247	466	174	88		314	20	152	350	130	160	106	198	131
ncbi gi g396376	g3218397	g2660670	g1717966 88		g2500938	g3153821	g1805251	g2388995	g4104400	g4200325	g562121	g3288594	g1175451
Database Hit ncbi gi g39637													
Selection Basis LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 332-359	807-827		453-479		487-511	607-629	430-457	747-774	717-741	587-606		457-476	447-466
Primer 5 pos 22-43	22-49		38-57		42-60	22-43	22-48	29-56	39-58	55-79		71-90	22-47
Seq Prime num Seq id Contig source 5 pos 23312 ENU07106 ANIGIC2433: 22-43	23313 ENU07107 ANI61C1524: 22-49 30222112	23314 ENU07108 ANI61C7026: 65750	23315 ENU07109 ANI61C7532: 38-57 27763178		23316 ENU07110 ANI61C9485: 42-60 21722716	23317 ENU07111 ANI61C339:1 22-43 110421	23318 ENU07112 ANI61C2444: 22-48 1043700	23319 ENU07113 ANI61C6363: 41455494	23320 ENU07114 ANI61C9995: 39-58 79840	23321 ENU07115 ANI61C244:2 55-79 2921664	23322 ENU07116 ANI61C1494: 40734386	37:	23324 ENU07118 ANI61C1547: 22-47 572260

Seq         Primer         Primer         Selection         Database Hit         Hit nebiginal         Sore         Sone Probation         % id cvrg           23325 ENUO71120 ANIGICTS76:         1,1NAP         Basis         Database Hit         Hit nebiginal         Sore         Sone Probator         % id cvrg           23325 ENUO7120 ANIGICTS76:         1,17372047         LINAP         g-4586315         104         57         0.0000000         29           23326 ENUO7121 ANIGICTS97:         22-43         790.809         LINAP         g-43136052         235         62         0.000000         29           23328 ENUO7122 ANIGICTS97:         27-46         379-397         LINAP         g-3136052         235         62         0.000000         0         34           23328 ENUO7122 ANIGICTS97:         37-37         LINAP         g-3406059         603         124         8.00E-55         52         61           23330 ENUO7124 ANIGICCA97:         30-406059         603         124         8.00E-55         52         61           23331 ENUO7125 ANIGICCA98:         10-4130         73-3-39         LINAP         g-2440206         79         10         10         7         55         61           23333 ENUO7127 ANIGICCA408:         <	Description stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata; (X85962) delta-9 fatty acid desaturase	[AJellomyces capsulatus] (AB010438) organic-cation transporter like 3 [Homo sapiens]	putative tartrate transporter; (U323/3) membrane protein [Agrobacterium vitis] (AL023592) acetamidase	[Schizosaccharomyces pombe] (AL023776) hypothetical protein [Schizosaccharomyces pombe]	(AF017646) TFIIH subunit p47 [Schizosaccharomyces pombe]; (AL031525) tfiih subunit p47. [Schizosaccharomyces pombe]	suppressor protein SEF1; (U92898) suppressor protein [Kluyveromyces lactis]	(AF027868) YocH [Bacillus subtilis]; (Z99114) similar to cell wall-binding protein [Bacillus subtilis]	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium]	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]	(AL023589) membrane transporter [Schizosaccharomyces pombe]	(M36482) SNF5 protein [Saccharomyces cerevisiae]
Selection         aat Basis         Blast Score         Blast Score         Blast Score         Prob Prob Do           LINAP         g4586315         104         57         0.000000           LINAP         g4033481         224         110         1.00E-23           LINAP         g3136052         235         62         0.000000           LINAP         g3406059         603         124         8.00E-55           LINAP         g2619050         97         56         0.000000           LINAP         g2440206         793         103         1.00E-21           LINAP         g2440206         307         136         8.00E-32           LINAP         g3135990         1070         171         4.00E-42           LINAP         g3135990         1070         171         4.00E-42	% cvrg 21	29	34	16	61	23	55	12	21	46	21
Selection         aat g1078614         Blast 212         Score 96           LINAP         g4586315         104         57           LINAP         g3136052         235         62           LINAP         g3184062         240         59           LINAP         g3406059         603         124           LINAP         g2619050         97         56           LINAP         g2440206         793         103           LINAP         g2440206         307         136           LINAP         g3135990         1070         171           LINAP         g3135990         1070         171           LINAP         g172638         430         153	% id	28	33	31	. 52	26	27	27	33	49	5 42
Selection         aat           Basis         Database Hit         ncbi gi         Score           LINAP         g4586315         104           LINAP         g3136052         235           LINAP         g3184062         240           LINAP         g3184062         240           LINAP         g3184063         603           LINAP         g2619050         97           LINAP         g2440206         793           LINAP         g2440206         307           LINAP         g3135990         1070           LINAP         g3135990         1070           LINAP         g3135990         1070		0.000000	1.00E-23 0.000000	004 7.00E-19	8.00E-55	0.0004	0.000000	1.00E-21	8.00E-32	4.00E-42	1.00E-36
Selection Basis Database Hit LINAP		57	110	59	124	46	56	103			153
Selection Basis Database Hit LINAP	aat Score 212	104	235	240	603	169		793	307	1070	430
Selection Basis LINAP	ncbi gi g1078614	g4586315	g4033481 g3136052	g3184062	g3406059	g3024604	g2619050	g2147662	g2440206	g3135990	g172638
Seq id Contig source 5 pos 3 pos 5 pos 17372047  ENUO7119 ANIG1C7576: 17372047  ENUO7121 ANIG1C39:2 41-59 456-479 4652107  ENUO7122 ANIG1C9972: 22-43 790-809 12082292  ENUO7123 ANIG1C9992: 32-54 779-803 18701  ENUO7124 ANIG1C7593: 27-46 379-397 972357  ENUO7125 ANIG1C7578: 30-49 782-801 11212101  ENUO7125 ANIG1C3399: 97-119 708-731 25621  ENUO7128 ANIG1C6408: 40-59 809-829 2484889  ENUO7130 ANIG1C7586: 46-65 613-630 11711	Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Seq id Contig source 5 pos ENU07119 ANI61C7576: 17372047 ENU07120 ANI61C399.2 41-59 4652107 ENU07121 ANI61C9972: 22-43 1208259 ENU07122 ANI61C9992: 32-54 18701 ENU07123 ANI61C2437: 1456399 ENU07125 ANI61C7578: 30-49 11212101 ENU07126 ANI61C3399: 97-119 25621 ENU07128 ANI61C2439: 62-82 3181 ENU07129 ANI61C6408: 40-59 2484889 ENU07130 ANI61C7586: 46-65	Primer 3 pos	456-479	790-809	779-803		782-801	373-395	708-731	456-476	809-829	613-630
Seq id Contig source ENU07119 ANI61C7576: 17372047 ENU07120 ANI61C39:2 4652107 ENU07121 ANI61C9972: 1208257 ENU07122 ANI61C9992: 18701 ENU07123 ANI61C2437: 1456399 ENU07125 ANI61C7578: 11212101 ENU07126 ANI61C3399: 25621 ENU07127 ANI61C3399: 25621 ENU07128 ANI61C6408: 2484889 ENU07130 ANI61C7586: 11711	Primer 5 pos	41-59	22-43 27-46	32-54		30-49	104-130	97-119	62-82	40-59	46-65
Seq id ENUO71: ENUO71: ENUO71: ENUO71: ENUO71: ENUO71: ENUO71:		20 ANI61C339:2 4652107	21 ANI61C9972: 12082292 22 ANI61C7593:	972357 23 ANI61C9992: 18701	24 ANI61C2437: 1456399	25 ANI61C7578: 11212101	26 ANI61S1068: 4391	27 ANI61C3399: 25621	28 ANI61C2439: 3181	29 ANI61C6408: 2484889	30 ANI61C7586: 11711
Seq num 23325 23326 23327 23329 23330 23332 23333 23334 23335 23335 23336	ieq num Seq id 3325 ENU0711	3326 ENU0712	3327 ENU0712 3328 ENU0712	3329 ENU0712	:3330 ENU0712	:3331 ENU0712	:3332 ENU0712	:3333 ENU0712	3334 ENU0712	3335 ENU0712	13336 ENU071

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% cvrg Description 15 DNA-directed RNA polymerase II largest subunit (RNA polymerase II subunit 1); DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - fission yeast (Schizosaccharomyces pombe); (X56564) RNA polymerase II large subunit (Schizosaccharomyces pombe)			(ALU31349) conserved hypothetical protein [Schizosaccharomyces pombe]	(Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]	hypothetical 210.4 KD protein in GUT1-RIM1 intergenic region; hypothetical protein YHL030w - yeast (Saccharomyces cerevisiae); (U11583) YHL030w gene product [Saccharomyces cerevisiae]		SMP2 protein; SMP2 protein - yeast (Saccharomyces cerevisiae); (D01095) Smp2 protein [Saccharomyces cerevisiae]; (Z49705) Smp2p [Saccharomyces cerevisiae]; SMP2 gene [Saccharomyces cerevisiae]	(L40632) ankyrin 3 [Mus musculus]	
. <del>D</del>	32		38			. 17	30		_
Blast Prob 1.00E-90	1.00E-23 41	4.00E-35 48	9.00E-81 62	0.000000	1.00E-12	3.00E-59 84	5.00E-74 56	1.00E-15	29
Blast Score 333	80	119	300	58	74	228	212	84	
aat Score 2756	184	462	/53	50	336	604	773	182	9/
ncbi gi g548817	g4107287	g4200122	g3451474	g3875727	g731610	g3661614	g417782	g710551	
on Database Hit								,	
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 715-739	567-586	809-828	644-663	) 460-479	785-812	362-381	798-821	635-659	
Seq Primer num Seq id Contig source 5 pos 23337 ENU07131 ANI61C9493: 35-62 3165373	23338 ENU07132 ANI61C3414: 38-60 1630.2327	23339 ENU07133 ANI61C243:2 51-70	23340 ENU07134 ANI61C9478: 44-63 7211	23341 ENU07135 ANI61C2443: 118-140 460-479 4521	23342 ENU07136 ANI61C7019: 22-42 2157358	23343 ENU07137 ANI61C3440: 42-69 402795	23344 ENU07138 ANI61C2443: 24-46 36032148	23345 ENU07139 ANI61C9482: 24-46 33043985	23346 ENU07140 ANI61S138:9 67501

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	Description (AC006439) hypothetical protein [Arabidopsis thaliana]	(U91543) zinc-finger helicase [Homo sapiens]	(AL023554) fork head protein type transcription factor	[Schizosaccharomyces pombe] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [Schizosaccharomyces	(AL035085) putative mitochondrial carrier protein [Schizosaccharomyces nombel	(AB003310) chitin synthase regulatory factor [Candida albicans]	"phosphatidylinositol polyphosphate 5-phosphatase, isoform a; (U57627) oct 1 [Homo sapiens] "	(AL034563) putative polyA-binding protein. [Schizosaccharomyces pombe]	"citrate synthase, mitochondrial precursor; (AB001565) citrate synthase [Candida tropicalis] "	(AL021747) hypothetical protein [Schizosaccharomyces pombe]	(U59915) Noc1p [Schizosaccharomyces pombe]; (Z99568) noc1p. [Schizosaccharomyces pombe]	"glutamate decarboxylase (GAD); glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia; (L16797) glutamate decarboxylase [Petunia hybrida]; (L16977) glutamate decarboxvlase [Petunia hybrida] "	(AL049171) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana]
%	% id cvrg		38		39	38	Ξ	49	32	21		51	20
Blast	Prob 2.3	0.000000	8.00E-33 33	1.00E-10	9.00E-27 47	4.00E-46 42	0.000001 30	3.00E-16 29	2.00E-14 44	6.00E-38 46	0.023	4.00E-63 56	1.00E-10 37
Blast	Score 33	61	141	<i>L</i> 9	69	185	52	98	79	157	39	133	29
aat	Score 141	1004	463	29	332	546	65	170	199	360	79	935	83
	ncbi gi g4309732	g3298562	g3133109	g1351702	g4107480	g2073105	g4557813	g4049510	g2493724	g2842469	g1857082	g1169238	g4539416 82
	Database Hit ncbi gi g43097												
Selection	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 809-829	762-780	781-800	7 331-350	800-825		263-287	681-700		455-479	558-585	806-825	
Primer	5 pos 22-44	71-90	22-47	168-187	36-55		27-54	155-179		146-16	38-57	71-90	
Seq	num Seq id Contig source 23347 ENU07141 ANI61C342:2 543874	23348 ENU07142 ANI61C6406: 71-90	23349 ENU07143 ANI61C7015: 22-47 45953707	23350 ENU07144 ANI61S1513: 168-187 331-350 1553	23351 ENU07145 ANI61C3439: 36-55 8881	23352 ENU07146 ANI61C6426: 3111385	23353 ENU07147 ANI61C7062: 27-54 574267	23354 ENU07148 ANI61C7611: 155-179 681-700 23521355	23355 ENU07149 ANI61S187:3 02898	23356 ENU07150 ANI61C2463: 146-165 455-479 4251	23357 ENU07151 ANI61C6416: 38-57 42474853	23358 ENU07152 ANI61C7029: 71-90 41462624	23359 ENU07153 ANI61S2140: 234722

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	[Agrobactenum vius] (AL035637) putative alpha-glucan synthase [Schizosaccharomyces	hypothetical protein YPL181w - yeast (Saccharomyces cerevisiae); (Z73538) ORF YPL181w [Saccharomyces	"(AC004912) similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070) [Homo saniens] "	mitochondrial intermediate peptidase (EC 3.4.24) precursor - yeast (Saccharomyces cerevisiae); (Z28134) ORF YKL134c [Saccharomyces	Gephyrin (putative glycine receptor- tubulin linker protein); gephyrin - rat; (X66366) Gephyrin [Rattus	hypothetical 60.7 KD protein C30D11.08C in chromosome I; hypothetical protein SPAC30D11.08c - fission yeast (Schizosaccharomyces pombe); (Z67961) PHD finger protein [Schizosaccharomyces pombe]
% % id cvrg 30 24	10	29		21	20	37
Blast Prob 1.00E-16 3.00E-21	3.00E-74 59	0.00004 30	0.00009	1.00E-33 42	2.00E-14 36	4.00E-15 29
Blast Blast Score Prob 87 1.00E 101 3.00E	148	48	47	143	79	83
o o	734	117	38	323	110	128
aat ncbi gi Scor g479416 189 g4033486 200	g4481951 734	g2132222 117	g4263745	g539323	g417049	g1351661
Database Hit ncbi gi g47941 g40334						
Selection Basis LINAP LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer Primer 5 pos 3 pos 102-120 415-434 197-219 498-516	722-749	470-493	443-462	373-392	274-300	715-739
rimer i pos 02-120 97-219	14-68	22-48	22-49	22-45	28-49	24-46
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 23360 ENU07154 ANI61C2464: 102-120 415-434 4341 23361 ENU07155 ANI61C6433: 197-219 498-516 31532606	23362 ENU07156 ANI61C955:9 44-68 211	23363 ENU07157 ANI61C2468: 22-48 16562169	23364 ENU07158 ANI61C6422: 22-49 43824079	23365 ENU07159 ANI61C3420: 22-45 41614662	23366 ENU07160 ANI61S2566: 28-49 144575	23367 ENU07161 ANI61C7048: 24-46 28673715
Seq num 23360 23361	23362	23363	23364	23365	23366	23367

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Seq         Primer         Primer         Selection         Annum         Seq id         Primer         Primer         Selection         Annum         Seq id         Contig source         5 pos         3 pos         Basis         Datablase Hit nebi gi         Score         Score         Prob         % id         cvrg           2336         ENUOT165         ANIGLS269:1.         122-141         \$84-601         LINAP         g1679757         362         152         9.00E-40         39         30           23370         ENUOT165         ANIGLS269:1.         122-141         \$84-601         LINAP         g757832         235         \$5         2.00E-15         30           23370         ENUOT165         ANIGLS269:1.         122-141         \$84-479         LINAP         g201937         81         74         6.00E-13         33         58           23371         ENUOT165         ANIGLS268:2.2-48         454-479         LINAP         g1268849         144         56         5.00E-15         22         206-15         22         23373         ENUOT165         ANIGLS298:1.         149-168         291-318         LINAP         g2133266         311         97         8.00E-27         36         11           23375 </th <th>Description "FERRIC reductase transmembrane component 2 precursor; ferric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae); (X75950) ORF5, F711 [Saccharomyces cerevisiae]; (Z28220) ORF YKL220c [Saccharomyces cerevisiae]; ORF 5</th> <th>[Saccharomyces cerevisiae] " (U77605) two-component histidine kinase CHK-1 [Glomerella cingulata]; (U77606) two-component histidine</th> <th>Kinase Chr. 1 [Giomerena cingulata] (Z37980) hypothetical 4- hydroxyphenylacetate permease</th> <th>[Escuericina con] (M18209) transcription factor S-II [Mis musculus]</th> <th>(L77234) glycine rich protein (Neurospora crassa)</th> <th>(M80368) pathway-specific regulatory protein [Neurospora crassal</th> <th>chromosome scaffold protein sudA - Emericella nidulans; (U40146) chromosome scaffold protein</th> <th>[Emericella nidulans] maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z36167)</th> <th>ORF YBR298c [Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]</th> <th>(AL035523) putative protein [Arabidopsis thaliana]</th>	Description "FERRIC reductase transmembrane component 2 precursor; ferric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae); (X75950) ORF5, F711 [Saccharomyces cerevisiae]; (Z28220) ORF YKL220c [Saccharomyces cerevisiae]; ORF 5	[Saccharomyces cerevisiae] " (U77605) two-component histidine kinase CHK-1 [Glomerella cingulata]; (U77606) two-component histidine	Kinase Chr. 1 [Giomerena cingulata] (Z37980) hypothetical 4- hydroxyphenylacetate permease	[Escuericina con] (M18209) transcription factor S-II [Mis musculus]	(L77234) glycine rich protein (Neurospora crassa)	(M80368) pathway-specific regulatory protein [Neurospora crassal	chromosome scaffold protein sudA - Emericella nidulans; (U40146) chromosome scaffold protein	[Emericella nidulans] maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z36167)	ORF YBR298c [Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]	(AL035523) putative protein [Arabidopsis thaliana]
Seq id         Contig source         Primer         Selection         Basis         Database Hit nobi gi         ast         Blast         Blast           9 ENUO7162 ANIGLC7624: 29-56         453-479         LINAP         Basis         Database Hit nobi gi         Score         Frob         0.00001           9 ENUO7163 ANIGLC3621: 122-141         584-601         LINAP         g1679757         362         152         9.00E-40           1 ENUO7164 ANIGLC3451: 36-63         792-819         LINAP         g201937         81         74         6.00E-13           2 ENUO7164 ANIGLC3468: 22-48         454-479         LINAP         g201937         81         74         6.00E-13           2 ENUO7165 ANIGLC3468: 22-48         807-826         LINAP         g1568849         144         56         5.00E-11           2 ENUO7165 ANIGLC2481: 149-168         291-318         LINAP         g2133266         311         97         8.00E-27           3 ENUO7167 ANIGLC2481: 12-45         757-780         LINAP         g2342601         2446         157         3.00E-44           1 .3469         1 .3469         1 .74         6         157         3.00E-44           1 .7469-143         1 .104-168         291-318         LINAP         g24455254         <	% cvrg	30		28	28	22	11	45	5	16
Seq id 4231         Contig source 5 pos 4231         Primer 5 pos 453.479         Primer Basis LINAP         Selection Basis Basis LINAP         Database Hit g549758         at 1 670757         Blast 67         Score 5 50         Score 5 50           9 ENUO7163 ANIG1C7624: 29-56         453.479         LINAP         g1679757         362         152           1 ENUO7164 ANIG1C3451: 36-63         792-819         LINAP         g201937         81         74           20421199 20421199         1 ENUO7165 ANIG1C348: 22-45         807-826         LINAP         g1561823         944         122           2 ENUO7165 ANIG1C7056: 22-45         807-826         LINAP         g1561823         944         122           2 961992 2061992         3         LINAP         g201937         81         74           3 ENUO7165 ANIG1C7056: 22-45         801-820         LINAP         g234266         311         97           4 ENUO7169 ANIG1C248: 1 25-45         757-780         LINAP         g2342601         2446         157           5 ENUO7169 ANIG1C248: 1 25-45         757-780         LINAP         g2342601         2446         157           6 ENUO7170 ANIG1C3222: 1 25-43         136-161         276-294         LINAP         g2342501         81         94	% iq	39		33	36	29	89 (	7 23	38	74
Seq id         Contig source         5 pos         3 pos         Basis         Database Hit         nebi gi         Score           8 ENUO7162 ANIGIC7624: 29-56         453-479         LINAP         LINAP         g1679757         362           9 ENUO7163 ANIGIC369:1. 122-141         584-601         LINAP         g1679757         362           1 ENUO7164 ANIGIC3451: 36-63         792-819         LINAP         g1261937         81           2 ENUO7165 ANIGIC7468: 22-48         454-479         LINAP         g1261823         944           2 ENUO7165 ANIGIC7056: 22-45         801-826         LINAP         g1261823         944           2 ENUO7166 ANIGIC7056: 22-45         801-826         LINAP         g168849         144           2 ENUO7166 ANIGIC7056: 22-45         801-826         LINAP         g201337         444           3 ENUO7166 ANIGIC7248: 1.49-168         291-318         LINAP         g2133266         311           4 ENUO7169 ANIGIC248: 1.25-45         757-780         LINAP         g2342601         2446           5 ENUO7170 ANIGIC228: 1.36-161         276-294         LINAP         g4455254         181           560243         757-780         LINAP         g4455254         181		9.00E-40	2.00E-15	6.00E-13	4.00E-27	5.00E-1	8.00E-20	7.00E-17	3.00E-4	4.00E-19
Seq id Contig source 5 pos 3 pos Basis Database Hit 18 ENUO7162 ANI61C7624: 29-56 453-479 LINAP 1706  DENUO7163 ANI61S269:1. 122-141 584-601 LINAP 20421199  DENUO7164 ANI61C3451: 36-63 792-819 LINAP 20421199  DENUO7165 ANI61C2468: 22-48 454-479 LINAP 2061902  DENUO7166 ANI61C29538: 26-53 801-820 LINAP 2061902  DENUO7167 ANI61C9538: 26-53 801-820 LINAP 20831066  DENUO7169 ANI61C248:1 25-45 757-780 LINAP 3591  DENUO7170 ANI61C7021: 22-43 801-828 LINAP 3591  DENUO7170 ANI61C7021: 22-43 801-828 LINAP 3591  DENUO7171 ANI61S3228: 136-161 276-294 LINAP 569243		152	55	74	122	99	62	88	157	94
Seq id Contig source 5 pos 3 pos Basis Database Hit 18 ENUO7162 ANI61C7624: 29-56 453-479 LINAP 1706  DENUO7163 ANI61S269:1. 122-141 584-601 LINAP 20421199  DENUO7164 ANI61C3451: 36-63 792-819 LINAP 20421199  DENUO7165 ANI61C2468: 22-48 454-479 LINAP 2061902  DENUO7166 ANI61C29538: 26-53 801-820 LINAP 2061902  DENUO7167 ANI61C9538: 26-53 801-820 LINAP 20831066  DENUO7169 ANI61C248:1 25-45 757-780 LINAP 3591  DENUO7170 ANI61C7021: 22-43 801-828 LINAP 3591  DENUO7170 ANI61C7021: 22-43 801-828 LINAP 3591  DENUO7171 ANI61S3228: 136-161 276-294 LINAP 569243	aat Score 67	362	235	81	944	144	311	310	2446	181
Seq id Contig source 5 pos 3 pos Basis 8 ENUO7162 ANI61C7624: 29-56 453-479 LINAP 4231  1 ENUO7163 ANI61S269:1. 122-141 584-601 LINAP 20421199 20421199 20421199 2060.3004 2560.3004 2260.3004 2060.30	ncbi gi g549758	g1679757	g757832	g201937	g1261823	g168849	g2133266	g585446	g2342601	g4455254
Seq id Contig source 5 pos 3 pos 3 pos 4231  9 ENUO7163 ANI61C7624: 29-56 453-479 20421199  1 ENUO7164 ANI61C3451: 36-63 792-819 2660.3004  2 ENUO7165 ANI61C3451: 36-63 792-819 2660.3004  2 ENUO7166 ANI61C7056: 22-45 807-826 2961.992  3 ENUO7167 ANI61C9538: 26-53 801-820 20831066  4 ENUO7169 ANI61C248:1 25-45 757-780 3591  5 ENUO7170 ANI61C7021: 22-43 801-828 15469  7 ENUO7171 ANI61S3228: 136-161 276-294 569243										
Seq id Contig source 5 pos 8 ENU07162 ANI61S269:1. 122-141 .706  1 ENU07164 ANI61C3451: 36-63 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421199 20421066 ANI61C7056: 22-45 2961992 20831066 ANI61C248:1 25-45 3591 1.5469 201 25-43 1.5469 20243 2082136-161 569243	Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer lum Seq id Contig source 5 pos a de	Primer 3 pos 453-479	584-601	792-819	454-479	807-826	801-820	291-318	757-780	801-828	276-294
lum Seq id Contig source 13368 ENUO7162 ANI61C7624: 13369 ENUO7164 ANI61S269:1. 1370 ENUO7164 ANI61C2468: 20421199 2042199 20421199 2042.	Primer 5 pos 29-56	122-141	36-63	22-48	22-45	26-53	149-168	25-45	22-43	136-161
seq 13368 ENU07162 13369 ENU07164 13371 ENU07165 13372 ENU07166 13373 ENU07167 13374 ENU07170 13376 ENU07170	Contig source ANI61C7624: 4231	ANI61S269:1. .706	ANI61C3451: 20421199	ANI61C2468:	ANI61C7056:	ANI61C9538:	20031000 ANI61S298:1. .458	ANI61C248:1 3591	ANI61C7021:	ANI61S3228: 569243
	∞.	3369 ENU07163	3370 ENU07164	3371 ENU07165	3372 ENU07166	3373 ENU07167	3374 ENU07168	:3375 ENU07169	:3376 ENU07170	33 <i>77</i> ENU07171

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Seq Primer Primer Selection and Sequences from Sequences from Sequences from 3 poss Basis Database Hit nobi gi Score Score Prob % id cvrg 23378 ENUO7172 ANIGLS2548: 72-91 301-320 LINAP gi Sed5300 275 125 1.00E-28 44 34 34 234 23378 ENUO7173 ANIGLS2548: 72-91 301-320 LINAP gi Sed54529 217 89 2.00E-17 36 31 1.457	Description hypothetical 44.4 KD protein in CDC28-ARL1 intergenic region; SUR1 protein homolog YBR161w - yeast (Saccharomyces cerevisiae); (X80224) YBR1212 [Saccharomyces cerevisiae]; (Z36030) ORF YBR161w	[Out201] (U78597) kinesin light chain [Plectonema boryanum]  (AJ010981) putative transposase	[ I alaromyces stipitatus] conidial green pigment synthase; probable polyketide synthase - Emericella nidulans; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans]; wA	SIS2 protein (halotolerance protein HAL3); hal3 protein - yeast (Candida tropicalis); (X88900) hal3 [Candida protein]	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease	(Z99163) hypothetical protein [Schizosaccharomyces pombe]	(Z68119) cDNA EST EMBL:Z14951 comes from this gene; cDNA EST EMBL:T00215 comes from this gene; cDNA EST EMBL:D71583 comes from this gene; cDNA EST EMBL:D74238 comes from this gene; cDNA EST yk376f7.3 comes from this gene; cDNA EST yk376f7.3 comes from this
Spos         Selection         aat         Blast         Prob         72.0	% % % % % % % % % % % % % % % % % % %	31	41	19	40	70	
Primer         Selection         Basis         Database Hit         nebi gi         Score           72-91         301-320         LINAP         g2645229         275           134-153         290-312         LINAP         g3646479         198           26-45         722-749         LINAP         g549443         569           47-66         669-692         LINAP         g2498915         89           22-48         519-538         LINAP         g2408040         116           22-46         433-452         LINAP         g3879884         138	Blast Prob 1.00E-28	2.00E-17 36 7.00E-19 32	7.00E-55 39	0.000000 33	2.00E-24 31	0.000000 29	4.1
Primer         Selection         Spos         3 pos         Basis         Database Hit         ncbi gi           72-91         301-320         LINAP         g586300           134-153         290-312         LINAP         g2645229           143-169         414-441         LINAP         g3646479           26-45         722-749         LINAP         g549443           22-46         669-692         LINAP         g2498915           22-48         519-538         LINAP         g2408040           22-46         433-452         LINAP         g3879884	Blast Score 125	89	214	56	112	46	33
Primer 5 pos 3 pos 3 pos 3 pos 3 dasis 72-91       Basis 301-320       LINAP         134-153       290-312       LINAP         143-169       414-441       LINAP         26-45       722-749       LINAP         47-66       669-692       LINAP         22-48       519-538       LINAP         22-46       433-452       LINAP	aat Score 275	217	995	68	248	116	138
Primer         Primer         Selection           5 pos         3 pos         Basis           72-91         301-320         LINAP           134-153         290-312         LINAP           26-45         722-749         LINAP           47-66         669-692         LINAP           22-48         519-538         LINAP           22-46         433-452         LINAP           22-46         433-452         LINAP		g2645229 g3646479	g549443	g2498915	g125935	g2408040	g3879884
Primer Primer 5 pos 3 pos 72-91 301-320 134-153 290-312 143-169 414-441 26-45 722-749 22-48 519-538 22-46 433-452			,				
And Seq id Contig source 5 pos 3 pos 378 ENU07172 ANIG1C9548: 72-91 301-320 27312342	Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
94 Primer 1978 ENU07172 ANI61C9548: 72-91 1979 ENU07173 ANI61S3294: 134-153 11.457 1380 ENU07174 ANI61C2501: 143-169 11.479 1381 ENU07175 ANI61C3502: 47-66 1383 ENU07177 ANI61C3502: 47-66 1384 ENU07178 ANI61C252:1 22-48 1385 ENU07179 ANI61C553: 22-46 150.401	Primer 3 pos 301-320	290-312	722-749		669-692	519-538	433-452
am Seq id Contig source 378 ENU07172 ANI61C9548: 27312342 379 ENU07174 ANI61S3294: 1479 380 ENU07175 ANI61C2501: 1479 381 ENU07176 ANI61C3502: 278991 383 ENU07177 ANI61C3502: 278991 384 ENU07178 ANI61C252:1 513953 385 ENU07179 ANI61C7653: 750401	Primer 5 pos 72-91	134-153 143-169	26-45		47-66	22-48	22-46
yan nnn n n n	8 <del>8</del> 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	3379 ENU07173 ANI61S3294: 1457 3380 ENU07174 ANI61C2501:	1479 3381 ENU07175 ANI61C7017: : 10881	23382 ENU07176 ANI61S3549: 615290	3383 ENU07177 ANI61C3502: . 278991	3384 ENU07178 ANI61C252:1 513.953	3385 ENU07179 ANI61C7653: 750401

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Description suppressor protein SRP40; SRP40 protein - yeast (Saccharomyces cerevisiae); (X73541) ORF YKR412 [Saccharomyces cerevisiae]; (Z28317) ORF YKR920 [Saccharomyces	(AF035756) 2-dehydro-3-deoxyphosphoheptonate aldolase; phospho-2-dehydro-3-deoxyheptonate	autotase (Sureptontyces Sp.) (U28943) similar to ribitol dehydrogenase [Caenorhabditis	(AL049559) conserved hypothetical protein [Schizosaccharomyces pombe]	(D87895) chitinase [Emericella nidulans]	(AF001304) protease 1 [Pneumocystis carinii f. sp. carinii]	putative tartrate transporter; (U25634) putative tartrate transporter; inducible	by tartrate; Method: conceptual translation supplied by author. [Agrobacterium vitis]; ttuB gene [Agrobacterium vitis]	(AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa]	hypothetical 216.3 KD protein R06F6.8 in chromosome II; (Z46794) cDNA EST EMBL:T01654 comes from this gene; cDNA EST EMBL:D32326 comes from this gene; cDNA EST EMBL:D32810 comes from this gene; cDNA EST EMBL:D34680 comes from this gene; cDNA EST EMBL:D34680 comes from this gene; cDNA EST EMBL:D3556 comes from this gene; cDNA
% cvrg 54	18		48		12			48	∞
% id 21	44		47		4			28	35
Blast Prob 0.00004	0.00006	0.0002	8.00E-69 47	0.008	9.00E-18 44	6.00E-23		6.00E-15 28	4.00E-19 35
Blast Score 49	43	46	260	41	06	108		81	96
aat Score 101	61	69	695	102	181	225		157	140
ncbi gi g548976	g2687633	g861340	g4581524 695	g4063766 102	g2327061	g4033486 225		g2970667 157	g2496987 140
Database Hit ncbi gi g54897									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP
Primer 3 pos 793-814	301-323	459-478	804-829	661-682	259-280	692-714		299-318	798-817
Primer 5 pos 72-91	47-66	51-70	22-48	114-131	122-149	30-49		138-158	22-47
Seq Prime  13386 ENU07180 ANI61C9555: 72-91  1733899	23387 ENU07181 ANI61S3624: 47-66 1392	23388 ENU07182 ANI61C2550: 51-70 12491549	23389 ENU07183 ANI61C7020: 22-48 12962568	23390 ENU07184 ANI61C7660: 114-131 661-682 19901287	ANI61S3795: 122-149 259-280 3431	23392 ENU07186 ANI61C7664: 30-49 1735		23393 ENU07187 ANI61S4106: 138-158 299-318 4161	23394 ENU07188 ANI61C9570: 22-47 30841369
Seq num Seq id 23386 ENU07180	3387 ENU07181	3388 ENU07182	3389 ENU07183	3390 ENU07184	23391 ENU07185	3392 ENU07186		3393 ENU07187	3394 ENU07188
ν Ξ χ	%	73	7.	7,	2.	2.		2	7

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Description SIP3 protein; SIP3 protein - yeast (Saccharomyces cerevisiae); (U03376) Sip3p [Saccharomyces cerevisiae]; (X96722) ORF N0844 [Saccharomyces cerevisiae]; (Saccharomyces cerevisiae]	zinc finger protein GLI4 (neural specific DNA binding protein XGLI4) (XGLI-4); (U42462) neural specific DNA binding protein [Xenopus laevis]	A-agglutinin attachment subunit precursor; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae); (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae]; (Z71659) ORF YNR044w (Saccharomyces cerevisiae)	(Z99165) hypothetical protein [Schizosaccharomyces pombe]	(U59303) glucoamylase precursor [Aspergillus awamori]	(U/3443) alpha-amylase [Bacillus sp. MK 716]	HC-toxin synthetase (HTS); (M98024) HC-toxin synthetase [Cochliobolus carbonum]	(Z98741) oxidoreductase [Mycobacterium leprae]	hypothetical 73.1 KD protein C3H1.09C in chromosome I; (Z68144) major facilitator superfamily protein [Schizosaccharomyces pombe]	(Z50144) kynurenine/alpha- aminoadipate aminotransferase [Rattus norvegicus]	"(U66480) xylan beta-1,4-xylosidase [Bacillus subtilis]; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis] "
% cvrg			20	26		n	21	19		
Blast Prob % id 6.00E-16 32	1.00E-16	0.0002	1.00E-16 45	2.00E-27 50	0000000	1.00E-22 33	0.000000 32	2.00E-18 37	6.00E-12	1.00E-11
Blast Score 83	87	46	87	122	10	106	43	92	09	57
aat Score 159	125	84	189	380	69	212	88	194	110	303
2	g2501705	g416592			g166/4/4	g462367	g2342610	g1351692	g1050752	g1750122
n Database Hit ncbi gi g73074										
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 229-248	452-471	796-816	410-431	428-447	328-347	443-469	443-462	334-353	689-199	810-829
Primer 5 pos 87-106	72-91	24-43	46-65	22-45	32-51	61-85	118-137	33-53	56-75	48-75
Contig source 1189 ANI61S4269: 1380	23396 ENU07190 ANI61C2478: 72.91 21921830	23397 ENU07191 ANI61C7092: 24-43 92589	23398 ENU07192 ANI61C9586: 46-65 13581838		23400 ENU07194 ANI61S4557: 221599	07195 ANI61S4598: 61-85 4801	23402 ENU07196 ANI61C347:3 118-137 443-462 071	23403 ENU07197 ANI61S4611: 33-53 1391	23404 ENU07198 ANI61C2593: 56-75 1288568	23405 ENU07199 ANI61C3538: 48-75 1607354
Seq num Seq id 23395 ENUO	23396 ENU(	23397 ENU(	23398 ENU(	23399 ENU07193	23400 ENU(	23401 ENU07195	23402 ENU(	23403 ENU(	23404 ENU	23405 ENU

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	"(AF008220) SHCHC synthase [Bacillus subtilis]; (Z99119) 2- oxoglutarate decarboxylase and 2- succinyl-6-hydroxy-2,4- cyclohexadiene-1-carboxylate synthase	Ammonium transporter MEP2; ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae); (X83608) ammonium transporter [Saccharomyces cerevisiae]; (Z46843) NH3 permease [Saccharomyces cerevisiae]; (Z71418) ORF YNL142w	(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]	Bud site selection protein BUD6 (actin interacting protein 3); actin-interacting protein AIP3 - yeast (Saccharomyces cerevisiae); (U20618) Bud6p: actin interacting protein [Saccharomyces cerevisiae]; (U35668) Aip3p	(Z99107) similar to pet 112-like protein [Bacillus subtilis]	beta-glucuronidase - Escherichia coli; (Z32701) beta-glucuronidase [synthetic construct]
% cvrg 57	31	53	09	34	43	25
% id	49	4	5 54	3 37	65 (	0 62
Blast Prob % 3.00E-52 48	2.00E-40 49	8.00E-60 44	4.00E-66 54	2.00E-38 37	3.00E-50 59	6.00E-50 62
Blast Score 205	165	169	251	159	139	196
Score 447	370	725	707	432	462	457
ncbi gi g416820	g2293146	g1170922 725	g3281851 707	g1168699	g2632983	g541048
Database Hit ncbi gi g41682						
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos		790-809	791-810	802-829		375-394
5 pos		62-09	24-43	22-41		68-99
Seq num Seq id Contig source 5 23406 ENU07200 ANI61C7098: 13492123	23407 ENU07201 ANI61S53:1 551	23408 ENU07202 ANI61C2584: 60-79 11175	23409 ENU07203 ANI61C7071: 24-43 26721828	23410 ENU07204 ANI61C7679: 22-41 3611632	23411 ENU07205 ANI61S559:5	23412 ENU07206 ANI61C2598: 66-89 1460

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Description transcription factor NFATx - human; (U14510) NFATx [Homo sapiens] (D87671) TIP120 [Rattus norvegicus]	(297193) hypothetical protein Rv1894c [Mycobacterium tuberculosis] Aminoadipate-semialdehyde dehydrogenase large subunit (alpha-aminoadipate reductase) (alpha-AR); L-aminoadipate-semialdehyde dehydrogenase (EC 1.2.1.31) - yeast (Saccharomyces cerevisiae); (M36287) alpha-aminoadipate reductase (LYS2; EC 1.2.1.31) [Saccharomyces cerevisiae]; (X78993) alpha-aminoadipate reductase	[Saccharomyces cerevisiae]; (Z35984) ORF YBR115c [Saccharomyces cerevisiae]; (AD001531) alpha- aminoadipate reductase [Cloning vector pGR8] (Z78062) cDNA EST EMBL:D34090 comes from this gene; cDNA EST EMBL:D37114 comes from this gene; cDNA EST EMBL:D64639 comes from this gene; cDNA EST EMBL:D67728 comes from this gene; cDNA EST EMBL:C12617 comes	from this gene; cDN putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit; (U34740) putative fatty acid synthase alpha [Emericella nidulans]
% id cvrg 39 19	27	16	∞
% id 39	53	34	. 62
Blast Prob % 1 1 2.00E-27 39	0.000000 29 5 0.0000000 4	5.00E-18 34	1.00E-35 62
Blast Score 34 105	55	92	149
aat Score 492 680	63	147	336
aat ncbi gi Scor g2136300 492 g1799570 680	g126643 63	g3876027 147	g2492657 336
Database Hit ncbi gi g21363			
Selection Basis LINAP LINAP	LINAP	LINAP	LINAP
Primer 3 pos 807-828	249-272	691-710	
Primer 5 pos 22-45	30-51	22-44	
Seq Prime num Seq id Contig source 5 pos 23413 ENU07207 ANI61C355:3 22-45 0851963 23414 ENU07208 ANI61C7071:	23415 ENU07209 ANI61S577:1. 62-81 .314 23416 ENU07210 ANI61C7706: 30-51 1007584	23417 ENU07211 ANI61C3550: 22-44 33844143	23418 ENU07212 ANI61S77:33 81

# cecen name

Description hypothetical 56.6 KD protein in URE2-SSU72 intergenic region; hypothetical protein YNL223w - yeast (Saccharomyces cerevisiae); (Z69381) N1274 [Saccharomyces cerevisiae]; (Z71499) ORF YNL223w	[Saccharomyces cerevisiae] myoSIN-2 isoform; myosin myo2- yeast (Saccharomyces cerevisiae); (M35532) myosin 1 isoform (myo2) [Saccharomyces cerevisiae]; (Z75234) ORF YOR326w [Saccharomyces	cerevisiae] (U11098) hydroxyindole-O- methyltransferase [Homo sapiens]	"MG(2+) transport ATPase, P-type 1; (AE000495) Mg2+ transport ATPase, P-tyne 1 [Escherichia coli] "	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae); (Z73133) ORF YLL028w	protein kinase YAK1; protein kinase YAK1 (EC 2.7.1) - yeast (Saccharomyces cerevisiae); (X16056) Yak1 kinase (AA 1 - 807) [Saccharomyces cerevisiae]; (X87371) protein kinase [Saccharomyces cerevisiae]; (Z49417) ORF YJL141c	(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces nombel	(AL022022) PE_PGRS [Mycobacterium tuberculosis]
% id cvrg 40 42	12		Ξ	47	28	65	
% id 40	30	_	33	33	55	39	
Blast Prob % i 5.00E-10 40	1.00E-18 30	0.000000	4.00E-13 33	3.00E-37 33	8.00E-67 55	8.00E-13 39	0.1
Blast Score 60	94	19	74	155	206	73	37
aat Score 363	183	120	135	473	1005	195	42
ncbi gi g1730824	g127736	g607855	g728913	g2132651	g140201	g4539606	g2924449
Database Hit							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 802-829		457-479		794-813	766-785	360-380	452-476
Primer 5 pos 29-52		49-68		34-61	52-71	114-133	106-126
Seq Prime num Seq id Contig source 5 pos 23419 ENU07213 ANI61C7674: 29-52 33802309	23420 ENU07214 ANI61S79:1 595	23421 ENU07215 ANI61C7677: 49-68	23422 ENU07216 ANI61S816:1.	23423 ENU07217 ANI61C2621: 34-61 17313003	23424 ENU07218 ANI61C3547: 52-71 34281912	23425 ENU07219 ANI61C7112: 114-133 360-380 1425	23426 ENU07220 ANIGIC2637: 106-126 452-476 1497
Seq num Seq id 23419 ENU0721	23420 ENU0721	23421 ENU0721	23422 ENU0721	23423 ENU0721	23424 ENU072:	23425 ENU072.	23426 ENU072;

# obcara cana

% id cvrg Description 47 16 ATP-dependent bile acid permease;	probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae); (Z73153) ORF YLL048c [Saccharomyces cerevisiae]	3-isopropylmalate dehydratase (EC 4.2.1.33) - Phycomyces blakesleeanus; (X53090) alpha-isopropylmalate isomerase (AA 1-689) [Phycomyces hlakesleeanus]	"serine-type carboxypeptidase - Penicillium janthinellum; carboxypeptidase S3, penicillopeptidase S3, CPD-S3 [Penicillium janthinellum, IBT 3991, Peptide, 481 aa] "
% cvrg 16		40	24
% id 47		64	51
Blast Prob 3.00E-59		3.00E-96	115 1.00E-25 51
Blast Blast Score Prob 228 3.00E		351	115
aat Score 1425		1718	233
aat Blast Blast % ncbi gi Score Score Prob % id cvrg g3915963 1425 228 3.00E-59 47 16		g283065 1718 351 3.00E-96 64	g1363903 233
Database Hit ncbi gi g391596			
Selection Basis LINAP		LINAP	LINAP
Primer 3 pos 647-666		771-796	206-225
Seq Primer num Seq id Contig source 5 pos 23427 ENU07221 ANI61C7691: 22-47	26345362	23428 ENU07222 ANI61C8374: 29-48 361769	23429 ENU07223 ANI61S846:1. 68-89 .365

# cice company and some

70202020202020	[Plasposon plnMod-Klp] DNA-directed RNA polymerase I largest subunit; (Y09103) largest subunit of RNA polymerase I (A)	[Drosophila melanogaster] 60S ribosomal protein L3-2; ribosomal protein L3 - fission yeast (Schizosaccharomyces pombe); (X57734) ribosomal protein L3	[Schizosaccharomyces pombe] chromosome region maintenance protein 1; (X15482) crm1 product [Schizosaccharomyces pombe]
% id cvrg		53	26
	8	51 53	74 61
Blast Prob 9.00E-52	0.000000	1.00E-51 53	5.00E-74 61
Blast Score 203	57	117	225
aat 8Core 492	131	577	1580
ncbi gi g3135546	g3914818	g548771	g399299
Database Hit ncbi gi g31355			
Selection Basis LINAP	LINAP	LINAP	LINAP
Primer 3 pos 317-336			775-801
Primer 5 pos 28-48			23-45
Seq num Seq id Contig source 5 pos 23430 ENU07224 ANI61C8374: 28-48 19222257	ANI61S907:3 521	ANI61C7114: 4821158	23433 ENU07227 ANI61C7698: 23-45 31961151
9 m Seq id 430 ENU07224	23431 ENU07225 ANI61S907:3 521	23432 ENU07226 ANI61C7114: 4821158	433 ENU07227
Seq num 23433	23	23	23

# cicator caranta

Description quinate transporter); quinate permease (quinate transport protein - Emericella nidulans; (X13525) quinate permease Fimericella idulans!	probable malate oxidoreductase (NAD) (malic enzyme) (ME); malate dehydrogenase homolog YKL029c - yeast (Saccharomyces cerevisiae); (Z28029) ORF YKL029c	beta-glucan synthesis-associated protein KRE6; (D88490) CaKRE6	(AL023634) hypothetical protein (Schizosaccharomyces pombe)	(Y16675) aflatoxin B1-aldehyde reductase [Homo sapiens]	putative transporter YLL16C; probable membrane protein YLL16c - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces	cerevisiae] (AF030886) telomere-associated recQ-like helicase [Ustilago maydis]	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]	(AJ223998) PCZA361.18 [Amycolatopsis orientalis]	(AL023634) protein kinase dsk1 [Schizosaccharomyces pombe]	(AJ001909) transcriptional activator [Aspergillus niger]	(AJ223504) amino acid transporter [Amanita muscaria]	(X8942) peptide synthetase [Metarhizium anisopliae]
% id cvrg	38	21	21	78	37	36	2		37	13	45	2
-10	4.00E-46 40	2.00E-14 43	0.000000 27	2.00E-41 44	7.00E-40 47	2.00E-17 28	1.00E-20 33	3-13	4.00E-63 56	0.000000 29 2	3.00E-40 42	9.00E-49 40
Blast Prob 2.00E-10	4.00E	2.00E	0.000	2.00E	7.00F	2.00F	1.00F	4.00E-13	4.00I	0.000	3.001	9.00
Blast Score 66	130	51	55	107	108	06	74	75	241	99	131	194
aat Score 35	1218	179	77	463	414	173	220	70	1132	72	516	1597
ncbi gi g131768	g547888	g2498505	g3150252	g3378617	g731893	g2642224	g294845	g2894166	g3150261	g2808634	g4468097	g2342601
Database Hit												
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 454-475	802-829	536-563	456-479	806-828	682-703	796-815	702-729	453-479	768-786	432-451	770-789	712-730
Primer 5 pos 40-60	22-45	22-49	36-55	30-49	47-66	26-53	22-47	24-43	22-49	25-44	33-52	29-48
	23435 ENU07229 ANI61C2616: 22-45 26604618	23436 ENU07230 ANI61C7114: 22-49 39614544	23437 ENU07231 ANI61C7710: 36-55 2928. 3343	ANI61C2641:		23440 ENU07234 ANI61C7693: 26-53	79:	23442 ENU07236 ANI61C2649: 24-43	23443 ENU07237 ANI61C7110: 22-49 163643	23444 ENU07238 ANI61C8381: 25-44 355666	2655:	23446 ENU07240 ANI61C351:2 29-48 8221
Seq num Seq id Contig source 23434 ENU07228 ANI61C8392: 507884	435 ENU07229	436 ENU07230	437 ENU07231	23438 ENU07232	23439 ENU07233	440 ENU07234	441 ENU07235	442 ENU07236	443 ENU07237	444 ENU07238	445 ENU07239	446 ENU07240
Seq num 2343	23	23	23	23	23	23	23	23	23	23	23	23

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	C29E6.10C in chromosome I; (Z66525) unknown [Schizosaccharomyces pombe] hypothetical 57.3 KD protein GMC- type oxidoreductase CY50.03C; (Z77137) hynothetical protein Rv1279	[Mycobacterium tuberculosis] (U46857) vitellogenin [Anolis pulchellus] (D90917) eukaryotic protein kinase	[Synechocystis sp.] (D42138) PIG-B [Homo sapiens]	glycerate dehydrogenase (NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) (hydroxypyruvate dehydrogenase) (glyoxylate reductase) (HPR-A)	hypothetical 72.2 KD protein C12C2.05C in chromosome II; (Z54140) hypothetical protein ISchizosaccharomyces pombel	Pyrimidine pathway regulatory protein 1; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae); (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae]; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium]
% cvrg 23	27			78	25		12
% id 45	32			40	30	_	20
Blast Prob % 4.00E-11 45	6.00E-13 32	0.08	1.00E-11	7.00E-35 40	5.00E-16 30	0.000000	2.00E-53 50
Blast Score 69	74	37	71	147	84	61	209
aat Score 905	82	86 94	145	259	159	82	535
ncbi gi g1351624	g1723076	g1197667 g1653955	g1552169	g2494084	g1175425	g130784	g2147662
Database Hit ncbi gi							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 720-739	452-479	412-431	778-801	710-729	383-403	488-507	698-725
Primer 5 pos 22-44	42-69	60-79	99-85	25-44	32-56	32-54	36-55
9 <del>11</del>	11342760 23448 ENU07242 ANI61C8385: 42-69 39183469	23449 ENU07243 ANI61C7137: 60-79 1126763 23450 ENU07244 ANI61C8400: 45-64	13081782 23451 ENU07245 ANIGIC3600: 66-85 7681717	23452 ENU07246 ANI61C7678: 25-44 22081435	23453 ENU07247 ANI61C2687: 32-56 3761	23454 ENU07248 ANI61C3566: 32-54 53386011	23455 ENU07249 ANI61C7136: 36-55 8271
Seq id 47 ENU07241	48 ENU07242	49 ENU07243 30 ENU07244	51 ENU07245	52 ENU07246	53 ENU07247	54 ENU07248	55 ENU07249
Seq num 2344	2344	2344	2345	234;	234:	234;	234:

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	(X62570) IFP53 [Homo sapiens]	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum"	(AJ002894) OsGRP2 [Oryza sativa]	"Erythronolide synthase, modules 5 and 6 (ORF 3) (6-deoxyerythronolide B synthase III) (DEBS 3); 6-deoxyerythronolide B synthase III - Saccharopolyspora erythraea; (X62569) 6-deoxyerythronolide B synthase III [Saccharopolyspora erythraea]"	(AL031262) hypothetical protein [Schizosaccharomyces pombe]	"Ankyrin, brain variant 2 (ankyrin B)	"hypothetical 269.9 KD protein in FKH1-MET18 intergenic region; probable membrane protein YIL129c-yeast (Saccharomyces cerevisiae); (Z38059) orf, len: 2376, CAI: 0.14 (Saccharomyces cerevisiae] "	(L35053) endonuclease [Magnaporthe grisea]
	24	33		<b>∞</b>	57	6	11	23
% id 6 50	9 59	9 39	2	7 33	30	1 29	1 32	6 42
	3.00E-79 59	1.00E-19 39	2.00E-12	1.00E-27 33	0.73	0.000001 29	3,00E-31 32	1.00E-46 42
	295	95	43	123	35	53	136	187
aat Score 1429	1009	290	125	281	144	146	790	998
ncbi gi g136232	g32709	g3318897	g2624328	g2506137	g3417427	g231551	g731871	g522302
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 797-824	794-813	802-829	439-457			431-450	711-730	
Primer 5 pos 22-47	22-47	27-46	22-43			41-60	36-55	
Seq num Seq id Contig source : 23456 ENU07250 ANI61C7678: 51862864	23457 ENU07251 ANI61C3588: 22-47	23458 ENU07252 ANI61C2675: 27-46 2181168	23459 ENU07253 ANI61C8388: 22-43	54 ANI61C8388: 50013984	23461 ENU07255 ANI61C7738: 9411734	23462 ENU07256 ANI61C7743: 41-60	23463 ENU07257 ANI61C7740: 36-55 31371	23464 ENU07258 ANI61C8420: 11751
Seq num Seq id 23456 ENU0725	23457 ENU0725	23458 ENU0725	23459 ENU0725	23460 ENU07254 ANIGIC8388. 50013984	23461 ENU0725	23462 ENU0725	23463 ENU0725	23464 ENU0725

# ócetos centros

Description (Z98602) putative protein transport protein sec7 homolog	Nypothetical amino-acid permease in STE3-GIN10 intergenic region; probable transport protein YKL174c-yeast (Saccharomyces cerevisiae); (Z26878) unknown [Saccharomyces cerevisiae]; (Z28174) ORF YKL174c [Saccharomyces cerevisiae]; ORF Saccharomyces cerevisiae]	(Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]	(D90901) hypothetical protein [Synechocystis sp.]	(U41740) trans-Golgi p230 [Homo sapiens]; peripheral membrane protein p230 [Homo sapiens]	probable membrane protein YOR059c - yeast (Saccharomyces cerevisiae); (Z74967) ORF YOR059c [Saccharomyces cerevisiae]; (Z70678)	(AL023776) hypothetical protein [Schizosaccharomyces pombe]	(AL031187) putative protein [Arabidopsis thaliana]	guanine nucleotide-binding protein beta subunit-like protein (cross- pathway control WD-repeat protein CPC-2); CPC2 protein - Neurospora crassa; (X81875) CPC2 protein [Neurospora crassa]
% id cvrg 35 13		39	87		47		<b>∞</b>	55
% id 35		43	33		36		53	06
Blast Prob % i 2.00E-24 35	1.00E-13	9.00E-48 43	3.00E-31 33	0.031	7.00E-22 36	3.00E-14	2.00E-14 29	3.00E-71 90
Blast Score 113	51	171	136	39	104	78	79	268
aat Score 166	128	457	298	447	187	06	120	1460
aat ncbi gi Scor g2440190 166	g549738	g2330791	g1652017	g1213484 447	g2132871 187	g3184056 90	g3402751 120	g3023852 1460
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 608-632	713-732	646-673	784-809	805-829	686-713	452-479	424-448	740-759
Primer 5 pos 28-47	22-43	71-90	22-47	83-107	22-44	22-48	24-48	37-56
Contig source 5 ANI61C3612: 27491	ANI61C7168: 2 10751	ANI61C7739: 7	ANI61C3597: 2	ANI61C7150: 3212402	ANI61C8351: 2 90428303	ANI61C3638: 2	ANI61C7176: 2 19121502	ANI61C352:1 3
Seq Prime num Seq id Contig source 5 pos 23465 ENU07259 ANI61C3612: 28-47 7491	23466 ENU07260 ANI61C7168: 22-43 10751	23467 ENU07261 ANI61C7739: 71-90 7771	23468 ENU07262 ANI61C3597: 22-47 29212073	23469 ENU07263 ANI61C7150: 83-107 3212402	23470 ENU07264 ANI61C8351: 22-44 90428303	23471 ENU07265 ANI61C3638: 22-48 1001600	23472 ENU07266 ANI61C7176: 24-48 19121502	23473 ENU07267 ANI61C352:1 37-56 033711129

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Description "glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-Dglucan glucohydrolase); glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae); (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae]; (U30626) glucoamylase [Saccharomyces cerevisiae] and the statement of the st	hypothetical 57.0 KD protein in SOD2-RPL27 intergenic region; hypothetical protein YHR009c - yeast (Saccharomyces cerevisiae); (U10400)	(Z29098) transposase (putative) [Drosophila hydei]	(Z98763) putative Inositol polyphosphate phosphatase (Schizosaccharomyces nombel	hypothetical 49.3 KD protein C30D11.06C in chromosome 1; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein Schizosaccharomyces nombel	hypothetical 70.2 KD protein C22E12.10C in chromosome I; (Z70043) unknown	glycogen phosphorylase (EC 2.4.1.1) - yeast (Saccharomyces cerevisiae); (U28371) Glycogen phosphorylase (Swiss Prot. accession number P06738)	(Y17317) polyketide synthase [Aspergillus fumigatus]
% id cvrg	20		22	50	38	31	12
% id	) 53		2 46	0 32	t 51	2 56	3 27
Blast Prob 0.002	2.00E-19 53	4.00E-21	3.00E-52 46	0.000000 32	2.00E-54 51	3.00E-82 56	7.00E-23 27
Blast Score 43	96	102	175	49	212	305	108
Score 166	279	187	1186	124	999	1875	609
g728850	g731632	g436464	g2370558	g1351659 124	g1723522	g2117720 1875	g3163925
Database Hit ncbi gi g72885							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 739-758	459-479		805-823	806-829	703-725	709-736	803-829
Primer 5 pos 22-44	22-47		92-29	30-49	91-110	37-63	22-49
Seq id Contig source 4 ENU07268 ANI61C7151: 49114133	23475 ENU07269 ANI61C8436: 22-47 12251548	23476 ENU07270 ANI61C7182: 1867908	23477 ENU07271 ANIGIC7731: 57-76 12864662	23478 ENU07272 ANI61C3629: 30-49 42173351	23479 ENU07273 ANI61C3668: 91-110 1190445	23480 ENU07274 ANI61C3642: 37-63 29585308	23481 ENU07275 ANI61C7178: 22-49 2739278
Seq num 23474	2347	234	234′	234'	234′	234	234

# tatat e e e e e e e e e e e e

Description	(0+0+00) INIPS [FIORCUS IIIII ADIIIS]	(AJO11903) oxidoreduciase [Ciaviceps purpurea]	(AL031579) hypothetical protein [Schizosaccharomyces pombe]	methionyl aminopeptidase (EC 3.4.11.18) 2 - rat; (L10652) initiation factor 2 associated 67 kDa protein	[Rattus rattus] (Z99163) probable beta-adaptin	clatharin assembly protein [Schizosaccharomyces pombe] putative protein disulfide isomerase	C1F5.02 precursor; (Z68136) unknown (Schizosaccharomyces	pombe]	[Arabidopsis thaliana]	(AB005589) Srw1	[Schizosaccharomyces pombe] 2-haloalkanoic acid dehalogenase I (L-	2-haloacid dehalogenase I)	(halocarboxylic acid halidohydrolase I)	(EC 3.8.1.2) I - Pseudomonas sp;	(M62908) 2-haloalkanoic acid	dehalogenase I [Pseudomonas sp.] sericin MG-2 - greater wax moth	(fragments)	(AE001142) glutamyl-tRNA synthetase	(gltX) [Borrelia burgdorferi]	membrane efflux protein [Streptomyces coelicolor]
% % id cvrg 76 17	1 [	)	53	45	29	28	}			47	71							47	4	7
Blast Prob	9.00E-23 20	0.000003 27	0.031 33	2.00E-64 62	2.00E-12 30	0.000004 27		000000	60	1.00E-98 60	0.000000 27	7				90 0	) } ;	5.00E-50 44	2 OOE 12 26	07 71-700:7
Blast Score	) (	cc	39	167	73	52	ļ	ę	}	329	54					38	)	191	Ç	3
aat Score	153	104	74	1195		63	}	6	1	1072	91					136		622	196	2
o v			g3618210	g482458	g2408035 750	91352731		04567787		g2381494	g417106	)				01083944		g2688265	901 11791000	8400001
Database Hit ncbi gi																				
Selection Basis	LINAL	LINAL	LINAP	LINAP	LINAP	LINAP	! !	INAD		LINAP	LINAP					INAP		LINAP	TMAD	T T T T T T T T T T T T T T T T T T T
Primer 3 pos	783-801	701-718		804-829	804-829	460.483		770	400-473	807-829	448-467					307 50L	071-507	784-811	0	/10-/30
Primer 5 pos	104-123	94-113		22-46	34-53	73.45	<del>}</del>	,	04-77	22-45	48-67	; ?				21 50	00-10	22-41	;	<del>1</del> -C7
Seq num Seq id Contig source	23482 ENUO7276 AMBICO422: 3601299	23483 ENUO7277 ANIOTO8422: 94-113 701-718 4025.4843	23484 ENU07278 ANI61C843:1 1011990	23485 ENU07279 ANI61C7744: 22-46 40502553	23486 ENU07280 ANI61C8417: 34-53	12024 23487 FNI107281 ANIG1C3674: 23.45	5511	22400 ENTIO7302 ANTELCT744: 22 42	50175324	23489 ENU07283 ANI61C7767: 22-45	20933226 23490 ENU07284 ANI61C8444: 48-67	351673				23491 ENTIN7285 ANIGIC3654: 21 SA	2860.3613	23492 ENU07286 ANI61C7794: 22-41	1411267	30803830

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Description hypothetical 53.4 KD protein in SLT2- PUT2 intergenic region; hypothetical protein YHR036w - yeast (Saccharomyces cerevisiae); (U00062) Vh036um (Soccharomyces)	protein kinase DSK1 (DIS1- suppressing protein kinase); dis1- suppressing protein kinase dsk1 - fission yeast (Schizosaccharomyces pombe); (D13447) protein kinase	(295436) hypothetical protein Rv3633 [Mycobacterium tuberculosis] hypothetical 78.3 KD protein in RIP1-URA3 intergenic region; hypothetical	protein YEL023c - yeast (Saccharomyces cerevisiae); (U18530) Yel023cp [Saccharomyces cerevisiae] Topoisomerase 1-related protein TRF4	; topoisomerase I-related protein TRF4 - yeast (Saccharomyces cerevisiae); (Z48149) ORF [Saccharomyces cerevisiae]; (U31355) Trf4p [Saccharomyces cerevisiae]; (Z74857) ORF YOL115w [Saccharomyces	(AC000133) ORF [Emericella nidulans]	sodium/potassium-transporting ATPase alpha chain (sodium PUMP) (NA+/K+ ATPase); Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - white sucker; (X58629) adenosinetriphosphatase [Catostomus commersoni]	(L35601) ankyrin [Drosophila melanogaster]; ankyrin [Drosophila melanogaster]
%   cvrg   22	21	40	43			21	
Blast Prob % id 0.000000 28 004	2.00E-11 37	0.000000 29 6 0.000000 22 002	3.00E-36 35		0.000000	4.00E-18 36	2.00E-17
Blast Score 61	89	54	152		48	57	06
aat Score 102	601	69 261	299		265	221	387
ncbi gi g731649	g544191	g2105061 g731409	g1717744 299	1	g1870209	g114386	g557084
Database Hit ncbi gi g73164							
Selection Basis LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP
Primer 3 pos	364-389	455-477	611-630		289-099	676-701	762-789
Primer 5 pos	137-164	22-48	23-45		22-46	25-52	22-41
Seq num Seq id Contig source 3 23494 ENU07288 ANI61C7797: 1319	23495 ENU07289 ANI61C8443: 137-164 364-389 1410	23496 ENU07290 ANI61C3624: 22-48 73277005 23497 ENU07291 ANI61C3690: 22-49 19061	23498 ENU07292 ANI61C7806: 23-45	28371468	23499 ENU07293 ANI61C3682: 22-46 16842391	23500 ENU07294 ANI61C7809: 25-52 30083729	23501 ENU07295 ANI61C3648: 22-41 60024666

# ce e e e e e e e e e

Description chitin synthase (EC 2.4.1.16) C - Aspergillus fumigatus; (X94245) chitin synthase C [Aspergillus fumigatus] (U78597) kinesin light chain [Plectonema boryanum] (U41806) p60 [Homo sapiens]	(AC000133) ORF [Emericella nidulans] (AL035076) putative allantoate permease [Schizosaccharomyces pombe] (176556) antigen N54 [Neospora sp.]	SPT10 protein; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae); (L24435) SPT10 [Saccharomyces cerevisiae]; (Z49402) ORF YIL127c [Saccharomyces	(ALO31545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe] choline transport protein; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein	[Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae] (U58946) transposase [Aspergillus awamori] hypothetical protein YPR031w - yeast (Saccharomyces cerevisiae); (Z49274) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]
% cvrg 26 41 41	27 54	33	17	38
% id 66 37 31	92 30	33	42 29	40
Blast Prob 8.00E-71 2.00E-34 0.00005	2.00E-60 92 7.00E-28 30	4.00E-19 33	3.00E-16 42 2.00E-18 29	2.00E-39 40 1.00E-13
Blast Score 267 146	231 124 49	95	84	162
aat Score 2998 502		179	305	348 88 88
ncbi gi g2133248 g2645229 g1145799	g1870209 g4107287	g464786	g3581903	g1805251 g1084952
Database Hit				
Selection Basis LINAP LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 768-788 568-593 372-391	315-338 802-829	590-609	267-294	589-608
Primer 5 pos 32-51 37-56 27-45	22-44	102-120	24-44	28-51
Seq Primer and Primer and Primer and Contig source 5 pos 23502 ENU07296 ANIG1C7778: 32-51 75914646 75914646 53503 ENU07297 ANIG1C3644: 37-56 58416454 57-45	23505 ENU07299 ANI61C8492: 104-123 315-338 8281277 23506 ENU07300 ANI61C3677: 22-44 802-829 29901456	23508 ENU07302 ANIGLC3705: 102-120 590-609 1655	23509 ENU07303 ANI61C7845: 24-44 14091091 23510 ENU07304 ANI61C3693: 22-44 54916885	23511 ENU07305 ANI61C7850: 28-51 8141452 23512 ENU07306 ANI61C7862: 671286
Seq num Seq id 23502 ENU0729 23503 ENU0729	23505 ENU0725 23506 ENU0730	23508 ENU073C	23509 ENU073( 23510 ENU073(	23511 ENU073( 23512 ENU073(
Se 23 23 23 23	23 23 23	4 8	2 2 2	52 53

# the contact of the co

Description high-affinity glucoSE transporter; (U22525) high affinity glucose transporter [Kluyveromyces lactis] (AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe]; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe] (AL021409) polyketide synthase [Streptomyces coelicolor] probable membrane protein YDL133w - yeast (Saccharomyces cerevisiae); (X96876) putative ORF [Saccharomyces cerevisiae]; (Z74181) ORF YDL133w [Saccharomyces cerevisiae] aminopeptidase Y (EC 3.4.11) - yeast (Saccharomyces cerevisiae); (L31635) aminopeptidase Y (EC 3.4.11) - yeast (Saccharomyces cerevisiae) (Saccharomyces cerevisiae) (Saccharomyces cerevisiae) (Saccharomyces cerevisiae) (Saccharomyces cerevisiae) (Z69254) alpha-galactosidase [Hypocrea jecorina] (AF023132) choline monooxygenase (EC 1.13.11.43) III isozyme beta chain - Pseudomonas paucimobilis; (S80637) lignostilbene-alpha,beta-dioxygenase isozyme III, LSD-III	[Pseudomonas paucimobilis, TMY1009, Peptide, 489 aa] [Sphingomonas paucimobilis]"
% id cvrg 28 42 27 43 31 11 31 11 44 46	
% id 28 28 27 27 27 33 33 44 44	
Blast Prob % i 3.00E-23 28 6.00E-10 27 4.00E-24 31 2.00E-19 33 3.00E-54 3.00E-69 55 0.000000 03 1.00E-47 44	
Blast Score 72 72 65 65 65 48 48 189	
aat Score 364 202 202 601 183 542 542 447	
aat ncbi gi g1346290 364 g2981103 202 g2808753 601 g2132440 183 g584764 542 g2522210 111 g2120665 447	
Database Hit	
Selection Basis LINAP LINAP LINAP LINAP LINAP LINAP LINAP LINAP	
Primer 3 pos 807-829 807-829 366-385 366-385 712-731 449-476 686-713	
Primer 5 pos 48-72 63-82 22-44 22-44 24-51 24-51 24-50	
Contig source 1307 ANI61C7819: 14852608 1308 ANI61C3737: 1184287 1310 ANI61C3786: 9321412 9321412 11282120 1311 ANI61C3744: 8431 1313 ANI61C8510: 3106263 7314 ANI61C3730: 1373619	
Seq num Seq id 23513 ENUOT 23514 ENUOT 23515 ENUOT 23518 ENUOT 23519 ENUOT 23520 ENUOT	

# ciae e cie e a hener

Description (AL031545) muts family DNA mismatch repair protein	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum; Chain D, Phenol Hydroxylase From Phenol Hydroxylase From Trichosporon Cutaneum; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum; Chain Cha	Inchosporon Cutaneum DNA ligase I (polydeoxyribonucleotide synthase (ATP)); DNA ligase (ATP) (EC 6.5.1.1) I - mouse; (U19604) DNA ligase I [Mus musculus]; (U04674) DNA ligase I [Mus	"type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (5PTase); (M74161) inositol polyphosphate 5-	pnospnatase [Homo sapiens] myo-inositol transporter 2; (Z95334) Irr2n [Schizosaccharomyces nombe]	(U24167) PAKI [Saccharomyces cerevisiae]	(U41748) coded for by C. elegans cDNA yk16f8.5; coded for by C. elegans cDNA yk55f7.5; coded for by C. elegans cDNA yk16f8.3; coded for by C. elegans cDNA yk55f7.3; coded for by C. elegans cDNA yk72a5.5; coded for by C. elegans cDNA yk72a5.5;	yk / zaz. z "(AF029354) exo-beta-1,3-glucanase [Amnalomucae misomalis]"	Ferrichrome siderophore peptide synthetase; (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]
% cvrg 22	36	27	16	21	12		33	7
% id 44	31	38	36	26	46		45	30
Blast Prob % 7.00E-66 44	2.00E-14 31	9.00E-38 38	4.00E-19 36	0.000000 26	0.000000 46	3.1	4.00E-62 45	2.00E-28 30
Blast Score 250	80	157	95	56	42	32	238	92
aat Score 1423	95	916	224	69	847	51	722	282
ncbi gi g3581916	g3318897	g1352290	g1352493	g3219812	g862488	g1118141	g3004863	g3914984
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 803-829	799-817	774-793	443-462		620-637	438-457	794-813	620-643
Primer 5 pos 22-49	2-46	9-59	2-47		2-42	.2-47	3-50	22-44
Seq num Seq id Contig source 5 23521 ENU07315 ANI61C787:1 2 4183186	23522 ENU07316 ANI61C7869: 22-46 27371530	23523 ENU07317 ANI61C3743: 39-59 14663481	23524 ENU07318 ANI61C7892: 22-47 1050591	23525 ENU07319 ANI61C7898:	23526 ENU07320 ANI61C7913: 22-42	23527 ENU07321 ANI61C8507: 22-47 1205896	23528 ENU07322 ANI61C7899: 23-50	23529 ENU07323 ANI61C7929: 22-44 14612302

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Description "mitochondrial 60S ribosomal protein L3 precursor (YML3); ribosomal protein YmL3, mitochondrial - yeast (Saccharomyces, cerevisiae); (Z49211)	Mrlp3p [Saccharomyces cerevisiae] " (AF008228) odd Oz protein [Drosophila melanogaster]	"leucyl-TRNA synthetase, cytoplasmic (leucineTRNA ligase) (LEURS); leucinetRNA ligase (EC 6.1.1.4), cytosolic - Neurospora crassa; (M30473) leucyl-tRNA synthetase [Neurospora crassa]"	(AF017777) small optic lobes [Drosophila melanogaster]	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "	"cytochrome P450 XVIIA1 (P450-C17) (steroid 17-alpha-hydroxylase/17,20 lyase); steroid 17alpha-monooxygenase (EC 1.14.99.9)	cytochrome P450 I7 - rainbow trout; (X65800) steroid 17-alpha- monooxygenase [Oncorhynchus mykiss] "	probable membrane protein YOL060c - yeast (Saccharomyces cerevisiae); (X91067) 01216; hypothetical protein [Saccharomyces cerevisiae]; (Z74802) ORF YOL060c [Saccharomyces cerevisiae]	"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase); (L48994) exo-beta 1,3 glucanase [Cochliobolus carbonum]"	(Z98980) hypothetical protein [Schizosaccharomyces pombe]
% id cvrg 36 62	e .	15	7	25			37	26	25
% id ; 36	27	9	36	41	_		5 65	1 32	31
Blast Prob % i 5.00E-35 36	0.0001	9.00E-52 60	6.00E-11 36	3.00E-52 41	0.000007		1.00E-92 65	5.00E-21 32	3.00E-10 31
Blast Score 148	46	203	20	205	14		322	101	99
aat Score 322	49	240	110	840	95		1101	168	317
68,	_	g135140		g1166378	g231902		g2132836	g1352399 168	g2388984
Database Hit ncbi gi g13507									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP
Primer 3 pos 801-820	459-478	438-465	419-442	782-804	490-509		807-829	750-773	734-758
Seq Primer num Seq id Contig source 5 pos 23530 ENU07324 ANI61C8542: 68-87 1743828	23531 ENU07325 ANI61C8533: 58-77 34683161	23532 ENU07326 ANI61C7922: 24-51 47825315	23533 ENU07327 ANI61C8533: 81-103 4656.4194	23534 ENU07328 ANI61C8536: 66-85 33091177	23535 ENU07329 ANI61C858:8 24-45 72320		23536 ENU07330 ANI61C8544: 43-70 38612610	23537 ENU07331 ANI61C8586: 91-114 750-773 21161322	23538 ENU07332 ANI61C8567: 29-51 43906002

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	% id cvrg Description (AC000098) EST gb ATTS1136 comes from this gene. [Arabidopsis thaliana]	N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease - Neurospora crassa; (L34605) neutral amino acid permease [Neurospora crassa]	hypothetical 103.2 KD protein C24B11.10C in chromosome I; hypothetical protein SPAC24B11.10c - fission yeast (Schizosaccharomyces pombe); (Z67757) unknown Schizosaccharomyces pombel	putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe]	putative 90.2 KD zinc finger protein in CCA1-ADK2 intergenic region; hypothetical protein YER169w - yeast (Saccharomyces cerevisiae); (U18922) Yer169wp [Saccharomyces cerevisiae]	probable protein-tyrosine phosphatase YBR276C; probable protein-tyrosine- phosphatase (EC 3.1.3.48) - yeast (Saccharomyces cerevisiae); (X76053) YBR2013-ORF [Saccharomyces cerevisiae]; (Z36145) ORF YBR276c [Saccharomyces cerevisiae]; ORF YBR2013 [Saccharomyces cerevisiae]
%	cvrg	50			30	16
	% id	29			54	36
st	۹ 1	8.00E-18 29	6.00E-21	1.00E-16	2.00E-72 54	2.00E-17 36
Blast	: Prob 0.61	8.00	0.9	1.0		2.0
Blast	Score 35	91	100	87	164	68
aat	Score 133	236	160	82	813	66
	ncbi gi g2388584	g2507070 236	g1351653 160	g1351714	g731532	g586390
	Database Hit ncbi gi g23885					
Selection	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 810-829	167-791	436-457	806-827	748-769	391-413
Primer	5 pos 22-44	0-49	8-55	2-43	2-48	1-51
Seq	num Seq id Contig source 5 23539 ENU07333 ANI61C8567: 22 13813558	23540 ENU07334 ANI61C8572: 30-49 53306141	23541 ENU07335 ANI61C8570: 28-55 38973529	23542 ENU07336 ANI61C8596: 22-43 35312592	23543 ENU07337 ANI61C8593: 22-48 24313221	23544 ENU07338 ANI61C8552: 31-51 5161

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Description calcium-transporting ATPase 1 (GOLGI CA2+-ATPase); Ca2+- transporting ATPase (EC 3.6.1.38) PMR1 - yeast (Saccharomyces cerevisiae); (M25488) PMR1 protein [Saccharomyces cerevisiae]; (X85757) calcium transporting ATPase 1 [Saccharomyces cerevisiae]; (Z72690) ORF YGL167c [Saccharomyces	(AL035075) hypothetical TPR domain-containing protein	malic acid transport protein (malate permease); C4-dicarboxylate transport protein mae1 - fission yeast (Schizosaccharomyces pombe); (U21002) malic acid transport protein Cchizosaccharomyces pombe)	(U93874) cytochrome P450 102 [Bacillus subtilis]; (Z99117) similar to cytochrome P450 / NADPH- cytochrome P450 reductase [Bacillus	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum; (M37461) FAS2 protein [Penicillium patulum] "	(AJ223999) PCZA363.3 [Amycolatonsis orientalis]	hypothetical 54.3 KD TRP-ASP repeats containing protein C17H9.19C in chromosome I; (L75944) WD repeat protein [Schizosaccharomyces pombe]; (Z98597) beta-transducin [Schizosaccharomyces pombe]
% cvrg 25	18	35	17			4
% id 61	53	30	33		•	: 33
Blast Prob % 2.00E-71 61	3.00E-22 29	7.00E-21 30	1.00E-22 33	0.00000	0.000002	1.00E-16 33
Blast Score 269	106	100	106	62	42	87
aat Score 877	1329	184	139	105	81	283
ncbi gi g114301	g4107308 1329	g1708909 184	g1934614	g119830	g2894188	g3219975
Database Hit						
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 775-794	768-787	406-425	456-475	296-315	456-477	789-808
Primer 5 pos 23-47	23-46	56-75	11-61	39-59	52-71	72-92
Seq id Contig source 5 ENU07339 ANI61C8585: 61297445	23546 ENU07340 ANI61C86:53 23-46 0.4337	23547 ENU07341 ANI61C8621: 56-75 36873212	23548 ENU07342 ANI61C8630: 41-61 5841	23549 ENU07343 ANI61C864:1 39-59 337	23550 ENU07344 ANI61C8641: 52-71	23551 ENU07345 ANI61C8625: 72-92 11072494
Seq num 2354	23;	23.	23:	23.	23:	23.

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Description (Z69635) Similarity to Drosophila white protein (SW:WHIT_DROME); cDNA EST EMBL:M89346 comes from this gene; cDNA EST yk311f2.3 comes from this gene; cDNA EST yk311f2.5 comes from this gene (Caenorhabditis elegans)	hypothetical protein YLR074c - yeast (Saccharomyces cerevisiae); (Z73246) ORF YLR074c [Saccharomyces cerevisiae]	Serine/threonine protein phosphatase PP-X isozyme 1; phosphoprotein phosphatase (EC 3.1.3.16) X-1 (clone EP129) - Arabidopsis thaliana; (Z22587) protein phosphatase [Arabidopsis thaliana]; (AF030289) protein phosphatase X isoform 1 [Arabidopsis thaliana]; (AL035440) phosphoprotein phosphatase (PPX-1)	[Arabidopsis thaliana] hypothetical protein YLR423c - yeast (Saccharomyces cerevisiae); (U20939)	r if 4.2 sep [ baccharomyces cerevisiae] chromosome segregation protein CUT3; cut3 protein - fission yeast (Schizosaccharomyces pombe); (D30788) cut3 protein	Control ORF YKR039w  (Caneral amino-acid permease GAP1; amino acid transport protein GAP1 - yeast (Saccharomyces cerevisiae); (Z28264) ORF YKR039w	"(L76169) reverse transcriptase,	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae); (U10400) Ysc84p [Saccharomyces cerevisiae]
% cvrg 30	62		33	20	46	14	53
% id 5 43	3 37	_	4 26	5 24	1 40	9 31	5 42
Blast Prob % 1.00E-35 43	0.000000 37	2.00E-51	0.000004 26	4.00E-25 24	9.00E-51 40	4.00E-19 31	3.00E-36 42
Blast Score 108	55	201	52	98	200	94	=======================================
aat Score 350	116	1092	86	1899	474	135	394
ncbi gi g3876092	g2131767 116	g1346782	g1078089	g729230	g544369	g1166378	g626598
Database Hit				•			
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 703-730	458-476		449-468	771-793		436-463	802-829
Primer 5 pos 48-67	22-49		22-46	31-51		29-86	22-42
Seq num Seq id Contig source : 23552 ENU07346 ANI61C1037 4:37914541	23553 ENU07347 ANIGIC1038 3:48324388	23554 ENU07348 ANI61C1040 7:14181956	23555 ENU07349 ANI61C1040 2:23812038	23556 ENU07350 ANI61C43:32 31-51 06147	23557 ENU07351 ANI61C1041 4:1857	23558 ENU07352 ANIGIC1040	

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Description (AL049474) hypothetical protein	(U78597) kinesin light chain (Plectonema horvanum)	(U38821) pig1 [Magnaporthe grisea]	hypothetical 33.4 KD protein in MOEA-GRXA intergenic region precursor; (AE000185) putative asparaginase [Escherichia coli]; (D90720) Hypothetical protein in moeA-grxA intergenic region precursor. [Escherichia coli]; (D90721) Hypothetical protein in moeA-grxA intergenic region precursor. Intergenic region precursor.	hypothetical 32.5 KD protein in MSH6-BMH2 intergenic region; thioredoxin homolog YDR098c - yeast (Saccharomyces cerevisiae); (Z47746) probable thioredoxin [Saccharomyces	putative sulfate transporter YPR003C; probable membrane protein YPR003c- yeast (Saccharomyces cerevisiae); (Z48951) unknown [Saccharomyces cerevisiae]; (U31900) Lpz3p [Saccharomyces cerevisiae]; (Z71255)	(AF024618) cyclin H [Drosophila melanogaster]	putative dioxygenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
% cvrg 91	41	23	89	50	28	51	57
% id	37	25	38	51	36	30	4
Blast Prob 7.00E-12	5.00E-23 37	6.00E-11 25	2.00E-24 38	1.00E-32 51	7.00E-31 36	0.000000 30 02 25	2.00E-46 44
Blast Score 71	87	89	96	138	134	53	131
aat Score 180	241	111	265	314	212	222	613
ncbi gi g4538664	g2645229	g1055333	g2506204 265	g3025094 314	g1711596	g2570798	g2497056 613
Database Hit ncbi gi g45386							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 457-479	588-608	363-382	714-733	425-446	616-635	602-621	805-829
Primer 5 pos 51-70	22-48	45-64	22-47	45-64	24-43	22-47	47-66
Seq num Seq id Contig source 23560 ENU07354 ANIGIC1041	• •	4. 88 88	23563 ENU07357 ANI61C4349: 22-47 1384628	23564 ENU07358 ANI61C1042 . 5:27842396	23565 ENU07359 ANI61C1040 9:42174878	23566 ENU07360 ANI61C1043: 22-47 26003276 23567 ENU07361 ANI61C1038 47-65 8-91588406	23568 ENU07362 ANIGIC433:5 47-66 5236762

	Inke protein [Prodospora ansenna] (AL035159) putative oxidoreductase [Mycobacterium leprae] (Z99113) polyketide synthase [Bacillus subtilis] (U68040) polyketide synthase [Cochliobolus heterostrophus]	(X89442) peptide synthetase [Metarhizium anisopliae] (AL031825) putative membrane transport protein [Schizosaccharomyces	lipase 5 precursor; triacylglycerol lipase (EC 3.1.1.3) 5 precursor - yeast	(AJ224324) cp31BHv [Hordeum vulgare] (AF016585) polyketide synthase	module 6 [Streptomyces caelestis] alpha-glucosidase (maltase); (AF042494) alpha-glucosidase [Sulfolobus soffataricus]	(Z98602) putative protein transport protein sec7 homolog [Schizosaccharomyces pombe]	DNAJ protein; heat shock protein dnaJ - Clostridium acetobutylicum; (X69050) DnaJ [Clostridium acetobutylicum]	(AB008771) beta-N-Acetylglucosaminidase [Streptomyces thermoviolaceus]	(AL023517) putative secreted protease [Streptomyces coelicolor]
%   cvrg   42   11	33 9 10	8	24	∞		15	23		
Blast Prob % id 7.00E-16 37 2.00E-13 36	3.00E-10 34 6.00E-27 29 6.00E-54 43	9.00E-55 36 3.00E-19	3.00E-12 41	0.000000 7 2.00E-20 41	3.00E-18	1.00E-29 36	0.00001 35	0.000004	0.002
Blast Score 84 76	65 121 211	213	73	54	92	78	50	52	43
aat Score 124 166	123 189 275	1238	136	80	122	372	40	354	147
ncbi gi g3169083 g3023956	g4154042 123 g2634106 189 g1546072 275	g2342601 g3702646	g417253	g3550483 g2558841	g3912992	g2440190	g1169369	g3426176	g3130007
Database Hit									
Selection Basis LINAP LINAP	LINAP LINAP LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
3 pos 455-474 468-487	320-339 689-708 804-823	22-47 782-801 95-114 726-745	645-664	449-468	508-527	719-743	442-461	804-827	109-128 622-644
Primer 5 pos 22-49 67-86	70-89 38-57 29-48	22-47	110-137	48-73	51-70	25-45	23-46	22-45	109-128
Seq Primes 23569 ENU07363 ANI61C4387: 22-49 4151 23570 ENU07364 ANI61C4384: 67-86 15662087	23571 ENU07365 ANI61C1043 70-89 4:49984685 23572 ENU07366 ANI61C436:3 38-57 9213166 23573 ENU07367 ANI61C436:6 29-48 5705307	410: 5 402: 9	23576 ENU07370 ANI61C4429: 110-137 645-664 1704	1046 300 1444:	602208 23579 ENU07373 ANIGIC1044 1:37684364	23580 ENU07374 ANI61C4446: 25-45 1415392	23581 ENU07375 ANI61C1045 1:27022370	23582 ENU07376 ANI61C1100 0:23073900	23583 ENU07377 ANI61C1104 2:1321657
Seq num S 23569 E 23570 E	23571 E 23572 E 23573 E	23574 E 23575 E	23576 E	23577 E 23578 E	23579 E	23580 I	23581 1	23582 I	23583 1

## che e e e e e e e e e e e e e

Description (U57524) I kappa B alpha [Mus musculus]	"endoglucanase A precursor (endo-1,4-beta-glucanase A) (cellulase A); (L32742) cellulase [Caldocellum saccharolyticum] "	dedicator of cyto-kinesis 1; (D50857) DOCK180 protein [Homo sapiens]	(AC005966) Similar to gi 2829865 F316.4 from Arabidopsis thaliana BAC gb AC002396. [Arabidopsis thaliana]	(AB010810) phospholipase D [Candida albicans]	"methionyl-TRNA synthetase, cytoplasmic (methionineTRNA	ligase) (METRS); methioninetRNA ligase (EC 6.1.1.10), cytosolic - yeast (Saccharomyces cerevisiae); (Z73049) ORF YGR264c [Saccharomyces cerevisiae]; (Y07777) methioninetRNA ligase [Saccharomyces	retrograde regulation protein 2; RTG2 protein - yeast (Saccharomyces cerevisiae); (X94357) ORF NRF588; EMBL:SCRTG2X;M97691; PR:B44344;B44344 [Saccharomyces cerevisiae]; (M97691) Rtg2p [Saccharomyces cerevisiae]; (Z72774) ORF YGL252c [Saccharomyces	molybdopterin biosynthesis CNX1 protein (molybdenum cofactor biosynthesis enzyme CNX1); (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]; (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]
% cvrg 50	7	15	25	6	23		29	37
% id 36	28	26	37	37	72		36	45
Blast Prob 0.00009	0.00001	8.00E-22 26	0.000000 37	3.00E-26 37	2.00E-73 72		1.00E-12 36	3.00E-37 45
Blast Score 47	50	104	42	118	275		52	143
aat Score 89	81	109	124	417	663		150	347
35	g1708078	g4503355 109	g4249377 124	g3413518	g1711639		g1710803	g2497953
Database Hit ncbi gi g40973								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP
Primer 3 pos 277-300	401-419	804-829	457-479	432-452	501-525		404-423	782-803
Primer 5 pos 36-57	47-70	112-131	36-59	130-157	22-49		102-122	102-125
Seq Prime num Seq id Contig source 5 pos 23584 ENU07378 ANIGIC4476: 36-57 258558	104	23586 ENU07380 ANI61C4496: 112-131 804-829 1886	C1046 4589	23588 ENU07382 ANI61C439:1 130-157 432-452473	1C1102 14735		23590 ENU07384 ANI61C45:1 102-122 404-423 535	23591 ENU07385 ANI61C1046 102-125 782-803 8:1831

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"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger] "	probable membrane protein YDR205w - yeast (Saccharomyces cerevisiae); (Z68194) unknown [Saccharomyces cerevisiae]	hypothetical protein YDR332w - yeast (Saccharomyces cerevisiae); (U32517)	Ferric reductase transmembrane component 3 precursor; probable membrane protein YOR381w - yeast (Saccharomyces cerevisiae); (Z75289) ORF YOR381w [Saccharomyces	(AF033823) moira [Drosophila melanogaster]	hypothetical protein YLR116w - yeast (Saccharomyces cerevisiae); (U53877) Ylr116wp [Saccharomyces cerevisiae]; (X89514) putative orf [Saccharomyces cerevisiae]; (Z73288) ORF YLR116w [Saccharomyces cerevisiae]	histone H2A.1; histone H2A.1 - yeast (Saccharomyces cerevisiae); (V01304) histone H2A1 [Saccharomyces cerevisiae]; (U13239) histone H2A1 [Saccharomyces cerevisiae]; (Z48612) H2a1n [Saccharomyces cerevisiae]	(299531) ubiquitin system protein [Schizosaccharomyces pombe]
% 1 cvrg 38	33	40		16	31		
Blast Prob % id 0.000000 38 07	9.00E-28 43	7.00E-64 44	0.0002	7.00E-48 49	3.00E-26 46	2.3	0.13
Blast Score 45	124	244	46	169	8	33	37
aat Score 159	553			609	706	81	187
ncbi gi g1911486	g2132480 553	g2131433 692	g3913674 217	g4220848	g2131783	g121967	g2440180 187
Database Hit							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 454-479	805-825	800-827	810-829	764-783	452-479	801-828	535-558
Frimer 5 pos 22-49	40-59	22-42	22-48	26-45	55-79	24-42	178-202
Oontig source : ANI61C45:15	ANI61C4537: 4	ANI61C1046 5:2048718	ANI61C4532: ; 2747726	ANI61C1046 5:71036296			ANI61C5459: 1128550
Seq Prime num Seq id Contig source 5 pos 23592 ENU07386 ANI61C45:15 22-49 621195	23593 ENU07387 ANI61C4537: 40-59 12592507	23594 ENU07388 ANI61C1046 22-42 5:2048718	23595 ENU07389 ANI61C4532: 22-48 2747726	23596 ENU07390 ANI61C1046 5:71036296	23597 ENU07391	23598 ENU07392 ANI61C1047 8:27733779	23599 ENU07393 ANI61C5459: 178-202 535-558 1128550
Seq num 2359	23:	23;	23.	23.	23.	23.	23.

	[Saccharomyces cerevisiae] (AB025252) reverse transcriptase	(143704) ketoreductase [Streptomyces sp. C5]	(AC004392) Contains similarity to gb[U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus [Arabidonsis thaliana]	(AF111172) lysosomal pepstatin insensitive protease precursor [Mus musculus]	Transmission-blocking target antigen S230 precursor; transmission-blocking target antigen Pfs230 - Plasmodium falciparum; (L08135) Pfs230 [Plasmodium falciparum]; (L04162) s230 [Plasmodium falciparum]; (AE001393) transmission blocking target antigen Pfs230 [Plasmodium	falciparum] (AL021046) putative mitotic spindle	"Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1; (L43920) microsomal omega-6 desaturase [Glycine max]"	lymphocyte specific helicase - mouse; (U25691) lymphocyte specific helicase [Mus musculus]
	57		50	17		19	59	4
	32		30	33		27	4	50
	2.00E-17	3.00E-13	4.00E-12	0.00005	0.000004	4.00E-28	8.00E-47	1.00E-70 50
	68	75	72	46	52	125	187	266
Score 121	133	108	96	285	118	297	371	700
ncbi gi g1710802	g4586458	g1163927	g3367519	g4106913	g730413	g2706463	g1345976	g2137490 700
Database Hit								
Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
3 pos 455-479	457-479	499-525	750-773	810-829	716-735	803-829	902-689	809-829
5 pos 68-95	22-46	22-49	22-49	62-88	51-70	22-48	23-49	22-49
num Seq id Contig source 23600 ENU07394 ANI61C1103 2:60456458	23601 ENU07395 ANI61C532:4	103	23603 ENU07397 ANI61C532:1	23604 ENU07398 ANI61C4578: 20401151	23605 ENU07399 ANI61C5492: 1785	23606 ENU07400 ANI61C5469:	07 43	23608 ENU07402 ANI61C4539: 22-49 37795452
	Seq id Contig source 5 pos 3 pos Basis Database Hit ncbi gi Score Score Prob % id cvrg DENU07394 ANIGLC1103 68-95 455-479 LINAP g1710802 121 75 3.00E-13 35 45 2:60456458	Seq id         Contig source         5 pos         Basis         Database Hit         ncbi gi         Score         Score         Prob         % id         cvrg           0 ENU07394 ANIGLC1103         68-95         455-479         LINAP         g1710802         121         75         3.00E-13         35         45           2:60456458         1         3.00E-13         35         45         45           1 ENU07395         ANIGLC532:4         22-46         457-479         LINAP         g4586458         133         89         2.00E-17         32         57	Seq id       Contig source       5 pos       Basis       Database Hit       ncbi gi       Score       Score       Prob       % id       cvrg         2 ENU07394 ANIGLC1103       68-95       455-479       LINAP       g1710802       121       75       3.00E-13       35       45         1 ENU07395 ANIGLC532:4       22-46       457-479       LINAP       g4586458       133       89       2.00E-17       32       57         1 ENU07396 ANIGLC1103       22-49       499-525       LINAP       g1163927       108       75       3.00E-13       57         2 ENU07396 ANIGLC1103       22-49       499-525       LINAP       g1163927       108       75       3.00E-13	Seq id       Contig source       5 pos       Basis       Database Hit       ncbi gi       Score       Score       Prob       % id       cvrg         2 ENU07394 ANIGLC1103       68-95       455-479       LINAP       LINAP       g1710802       121       75       3.00E-13       35       45         1 ENU07395 ANIGLC532:4       22-46       457-479       LINAP       g4586458       133       89       2.00E-17       32       57         2 ENU07396 ANIGLC1103       22-49       499-525       LINAP       g1163927       108       75       3.00E-17       32       57         3 ENU07397 ANIGLC532:1       22-49       750-773       LINAP       g3367519       96       72       4.00E-12       30       20         119511988       119511988       300E-12       30       20       20       20	Seq id       Contig source       5 pos       3 pos       Basis       Database Hit       ncbi gi       Score       Score       Prob       % id cvrg         2 ENU07394 ANIGICI103       68-95       455-479       LINAP       g1710802       121       75       3.00E-13       35       45         1 ENU07395 ANIGICS32:4       22-46       457-479       LINAP       g4586458       133       89       2.00E-17       32       57         2 ENU07396 ANIGICI103       22-49       499-525       LINAP       g1163927       108       75       3.00E-17       32       57         3 ENU07397 ANIGICS32:1       22-49       750-773       LINAP       g3367519       96       72       4.00E-12       30       20         119511988       119511988       810-829       LINAP       g4106913       285       46       0.00005       33       17	Seq id         Contig source         5 pos         3 pos         Basis         Database Hit         ncbi gi         Score         Score         Prob         % id         cvrg           2 ENU07394 ANIGICI103         68-95         455-479         LINAP         g4586458         133         89         2.00E-17         35         45           1 ENU07395 ANIGICS32:4         22-46         457-479         LINAP         g1163927         108         75         3.00E-17         32         57           2 ENU07395 ANIGICS32:1         22-49         499-525         LINAP         g1163927         108         75         3.00E-17         32         57           3 ENU07397 ANIGICS32:1         22-49         750-773         LINAP         g4106913         285         46         0.00005         33         17           4 ENU07399 ANIGICS492:         51-70         716-735         LINAP         g4106913         285         46         0.000005         33         17           20401151         1785         LINAP         g730413         118         52         0.0000004         33         17	Seq id         Contig source         5 pos         3 pos         Basis         Database Hit         nebi gi         Score         Score         Prob         % id         cvrg           D ENU07394 ANIGICS12.4         455-479         LINAP         g4586458         131         89         2.00E-13         35         45           1 ENU07395 ANIGICS12.4         22-46         457-479         LINAP         g4586458         133         89         2.00E-17         2         45           2 ENU07395 ANIGICS32.1         22-49         499-525         LINAP         g3367519         96         72         4.00E-12         30         20           3 ENU07397 ANIGICS478:         62-88         810-829         LINAP         g4106913         285         46         0.000005         33         17           20401151         5         716-735         LINAP         g730413         118         52         0.000004         77           5 ENU07400 ANIGICS492:         51-70         716-735         LINAP         g730413         118         52         0.000004         77	Seq id         Contig source         5 pos         Basis         Database Hit         in cbi gi         Score         Score         Prob         % id         cvg           DENUO7394         ANIGICS103         68-95         455-479         LINAP         g1710802         121         75         3.00E-13         35         45           1 ENUO7395         ANIGICS32-4         22-46         457-479         LINAP         g4586458         133         89         2.00E-17         35         57           2 ENUO7395         ANIGICS32-1         22-46         457-479         LINAP         g4366458         133         89         2.00E-17         57           3 ENUO7397         ANIGICS32-1         22-49         499-525         LINAP         g4367519         96         72         4.00E-12         30         20           1 ENUO7397         ANIGICS478:         62-88         810-829         LINAP         g736413         118         52         0.000005         33         17           5 ENUO7399         ANIGICS492:         51-70         716-735         LINAP         g736413         118         52         0.000004         17           6 ENU07400         ANIGICS469:         23-48         803-829

## ngunuso sosoo

Description probable serine/threonine-protein kinase C24B11.11C; hypothetical protein SPAC24B11.11c - fission yeast (Schizosaccharomyces pombe); (Z67757) unknown	cell division control protein 18; cell division control protein CDC18+-fission yeast (Schizosaccharomyces pombe); (L16793) cell division cycle protein [Schizosaccharomyces pombe]; (AL022305) cell division control protein 18 [Schizosaccharomyces pombe]	(AF096285) serine-threonine kinase receptor-associated protein [Mus musculus]	hypothetical 124.0 KD protein in PCS60-ABD1 intergenic region; probable membrane protein YBR235w - yeast (Saccharomyces cerevisiae); (Z36104) ORF YBR235w [Saccharomyces cerevisiae]	alpha-glucosidase precursor (maltase); (D45356) alpha-glucosidase [Aspergillus niger]	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]	hypothetical 22.2 KD protein C17G8.03C in chromosome I; (Z69795) unknown [Schizosaccharomyces pombe]	(Y18863) Pop4 protein [Homo sapiens]	(X89442) peptide synthetase [Metarhizium anisopliae]
% id cvrg 53 43	40	30	15	10	37	57		
Blast Prob 3.00E-54	5.00E-37 39	7.00E-10 53	1.00E-44 56	0.000000 37	0.000000 31	2.00E-20 47	9.00E-12	0.000000
Blast Score 201	155	61	137	61	57	66	71	59
aat Score 638	446	174	474	109	96	204	43	95
ncbi gi g1346360	g1168808	g4063383	g586352	g3023267 109	g4104775	g1723476	g4493697	g2342601
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 776-798	810-829	411-437	360-379	444-463	550-574	431-453	116-135 469-488	801-828
Primer 5 pos 24-47	22-49	57-83	22-45	55-72	22-40	45-64	116-135	36-55
		ANI61C4614: 1458	ANI61C5521: 4551028	ANI61C4601: 3301	ANT61C5535: 388982	887481	ANI61C1049 4:32262619	ANI61C5529: 1940700
Seq num Seq id Contig source 23609 ENU07403 ANI61C5517: 8761	23610 ENU07404 ANI61C1048 2:27614048	23611 ENU07405 ANI61C4614: 57-83 1458	23612 ENU07406 ANI61C5521: 22-45 4551028	23613 ENU07407 ANI61C4601: 55-72 3301	23614 ENU07408 ANI61C5535: 22-40 388982	23615 ENU07409 ANI61C4618: 45-64 887481	23616 ENU07410 ANI61C1049 4:32262619	23617 ENU07411 ANI61C5529: 1940700

## COLUCE CELOPO

Description "probable zinc metallopeptidase C17A5.04C precursor; (Z98849) probable zinc metallopeptidase, disintegrin [Schizosaccharomyces nombel."	"putative 151.3 KD transcriptional regulatory protein; probable membrane protein YLR278c - yeast (Saccharomyces cerevisiae); (U17243) Serine, glutamine, asparagine rich central portion of protein	(AL031107) putative secreted glucosidase [Streptomyces coelicolor]	(AB018321) KIAA0778 protein [Homo sapiens]	(AL031536) fnx1p. [Schizosaccharomyces pombe]	(U66283) dihydropteroate synthase [Pneumocystis carinii f. sp. muris]	(Z99708) putative protein [Arabidopsis thaliana]	(Y09899) sensory histidine protein kinase [Calothrix viguieri]	pyrroline-5-carboxylate reductase (P5CR) (P5CR) (F5 reductase); pyrroline-5-carboxylate reductase (EC 1.5.1.2) -Zalerion arboricola; (U33266) pyrroline carboxylate reductase	[Zalerion arboricola] (AB010714) salicylate hydroxylase	(AL009197) hypothetical ubiquitin conjugating enzyme	(Z82044) hypothetical 54.4 kd protein [Bacillus subtilis]
% cvrg	19	52	38		24	32	12	82	4	06	46
% id	7 31	34	1 37	~	48	33	38	34	3 31	3 49	0 30
Blast Prob % 3.00E-29 47	1.00E-27 31	5.00E-30 34	3.00E-24 37	6.00E-33	2.00E-61	0.00002	2.00E-11 38	3.00E-35 34	2.00E-23	1.00E-43 49	0.000000 30
Blast Score 128	123	131	112	141	235	49	69	149	109	168	47
aat Score 211	204	217	259	275	698	72	106	362	224	436	118
ncbi gi g3219959	g2501739		g3882277	g3560207	g2270900	g4006889	g2765035	g3024443 362	g2826168	g2661610	g1673402 118
Database Hit											
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 456-475	809-828	760-782	657-678	805-829	800-827		456-475	794-813	809-829	678-699	717-736
Primer 5 pos 37-56	22-48	26-49	37-57	22-44	38-57		22-43	22-49	22-42	23-50	25-44
Seq num Seq id Contig source 23618 ENU07412 ANI61C1106 5:65876241	23619 ENU07413 ANI61C8968: 22-48 9322028	23620 ENU07414 ANI61C1108: 26-49 38033001	23621 ENU07415 ANI61C4622: 2101318	23622 ENU07416 ANI61C5567: 22-44 11008	23623 ENU07417 ANI61C893:5 38-57 9644504	23624 ENU07418 ANIGIC1110 3:331652	23625 ENU07419 ANI61C1051 3:446782	23626 ENU07420 ANI61C1111 0:21851270	23627 ENU07421 ANI61C1047	• •	23629 ENU07423 ANI61C1107 3:25653336

	Description vegetatible incompatibility protein HET-E-1; (L28125) beta transducinlike protein [Podospora anserina]	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "	"(Z46869) exo-1,3-beta-glucanase/1,3-beta-D-Glucan glucanohydrolase	(Z99568) recombinational dna repair protein rhp55p. [Schizosaccharomyces pombe]; (AF053410) recombinational DNA repair protein Rhp55p	BTN1 protein; probable membrane protein YIL059w - yeast (Saccharomyces cerevisiae); (Z49334) ORF YIL059w [Saccharomyces	cerevisiae] (AJ012752) maltose permease [Saccharomyces cerevisiae]	(AJ224767) hypothetical protein [Acinetobacter sp. ADP1]	(U78597) kinesin light chain [Plectonema boryanum]	(AF043102) surface glycoprotein A [Pneumocystis carinii]	(Z99261) putative aminotransferase [Schizosaccharomyces pombe]	(AF019407) GTP-binding protein [Caulobacter crescentus]	(X03449) unidentified reading frame [Saccharomyces cerevisiae]
8	% id cvrg 54 20	12		40	41	20	71	49		55	27	79
	% id	34	<b>1</b> 0	32	7 40	8 38	0 23	6 35		8 38	0 45	0 36
Blast	Prob % 5.00E-81 54	1.00E-10 34	5.00E-15	0.003	3.00E-27 40	1.00E-18 38	0.000000 23	9.00E-36 35	99:0	4.00E-48 38	0.000000 45 05	0.000000 36 004
Blast	Score 282	99	81	34	121	92	61	150	35	191	58	62
aat	Score 1264	109	134	108	275	193	95	365	149	613	234	204
	ncbi gi g3023956	g1166378	g1150442 134	g2462678 108	g1352987	g3901117	g2959337	g2645229	g3184386 149	g2414656 613	g2555098	g3489
	Database Hit ncbi gi g30239											
Selection	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 660-679	366-385	460-487	387-406	335-357	314-333	426-445	799-817	680-703	620-643	308-332	464-483
Primer	5 pos 22-45	36-63	35-54	54-73	22-49	48-70	35-55	9-05	38-57	22-46	87-111	22-40
Seq	Seq id Contig source Contig Source COU CO COUNTY CO	23631 ENU07425 ANI61C558:1 36-63	1C1107 89147	23633 ENU07427 ANI61C1050 9:26513170	23634 ENU07428 ANI61C5640: 22-49 52717	23635 ENU07429 ANI61C8997: 48-70 1040656	23636 ENU07430 ANI61C4607: 27252293	23637 ENU07431 ANI61C5576: 5415.4439	66 92	<u>.</u> .	539:	1109

	Description probable electron transfer flavoprotein- ubiquinone oxidoreductase precursor (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (electron-transferring-flavoprotein dehydrogenase); hypothetical protein YOR356w - yeast (Saccharomyces cerevisiae); (Z75264) ORF YOR356w	phosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (Drosophila melanogaster); (U13014) phosphorylase kinase gamma	(Y17317) polyketide synthase	Diatom spindle kinesin 1; (U51680) diatom spindle kinesin 1 [Cylindrothecs fusiformis]	(235639) cDNA EST CEMSD23F comes from this gene; cDNA EST CEESE24F comes from this gene; cDNA EST from this gene; cDNA EST EMBL:D3566 comes from this gene; cDNA EST EMBL:D36562 comes from this gene; cDNA EST	(X69481) GTPase [Saccharomyces cerevisiae]	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]
8	% id cvrg 59 44		13	21		49	
	% id		5 29	38		32	
Blast	Prob % i 4.00E-96 59	3.00E-28	7.00E-25 29	4.00E-10 38	0.054	3.00E-29 32	0.00007
Blast	Score 351	93	114	65	39	129	47
aat	Score 1342	326	307	113	153	289	53
	346	g2133702	g3163925 307	g2497529 113	g4008344 153	g4006	g3236237
	Database Hit ncbi gi g24983						
Selection	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 721-740	805-827	762-780	453-479	776-795	625-644	457-479
Primer	5 pos 22-47	22-48	49-67	22-42	22-45	46-65	23-42
Seq	Seq id Contig source 12 ENU07436 ANI61C1051 5:14401	23643 ENU07437 ANI61C460:5 22-48 2534307	23644 ENU07438 ANI61C4647: 49-67	1051	23646 ENU07440 ANI61C8980: 22-45 38122877	23647 ENU07441 ANI61C5655: 46-65 6361524	113

## cerebi nebi

Description "beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase); xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Butyrivibrio fibrisolvens; (M55537) beta-D-xylosidase/alpha-L-arabinofuranosidase [Butyrivibrio fibrisolvens]	(L77083) cdc2 gene product [Nicotiana tabacum] (AE001274) MCAK; L549.3	acetylcholinesterase precursor (ACHE)	hypothetical 68.8 KD protein in EXO70-ARP4 intergenic region; hypothetical protein YIL083w - yeast (Saccharomyces cerevisiae); (X88851) hypothetical protein [Saccharomyces cerevisiae]; (X83502) J1002 [Saccharomyces cerevisiae]; (Z49358) ORF YIL083w [Saccharomyces	"Nucleoporin NUP159 (nuclear pore protein NUP159); nucleoporin RAT7-yeast (Saccharomyces cerevisiae); (Z38125) orf, len: 1460,CAI: 0.15 [Saccharomyces cerevisiae]; (L40634) nucleoporin [Saccharomyces	Lysosomal pro-X carboxypeptidase precursor (prolylcarboxypeptidase) (PRCP) (proline carboxypeptidase) (angiotensinase C) (lysosomal carboxypeptidase C); lysosomal Pro-X carboxypeptidase (EC 3.4.16.2) - human; (L13977)
% id cvrg 35 52		29	24	10	33
Blast Prob 5.00E-20	0.000000 007 2.00E-12	4.00E-16 40	7.00E-20 38	3.00E-13 34	3.00E-14 34
Blast Score 99	61	85	79	75	79
aat Score 188	96	212	184	83	107
ncbi gi g1175036	g1377890 g2978452	g543754	g1352996 184	g731862	g1172047 107
Database Hit ncbi gi g11750					
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 806-828	457-479	626-652	611-630	457-477	161-182 639-658
Primer 5 pos 23-42	46-65	23-42	34-53	22-42	161-182
Contig source ANI61C5641: 22341359	ANI61C8978: .14841879 ANI61C1051			ANI61C8986: 26203097	
Seq num Seq id 23649 ENU07443	23650 ENU07444 ANI61C8978: 46-65 14841879 23651 ENU07445 ANI61C1051 22-47	23652 ENU07446 ANI61C4646:	23653 ENU07447 ANIGICI110 0:33302673	23654 ENU07448 ANI61C8986: 22-42 26203097	23655 ENU07449 ANI61C1052 5:56334932

Description "aconitate hydratase, mitochondrial precursor (citrate hydro-lyase) (aconitase); (Z98601) aconitate hydratase. [Schizosaccharomyces	(AL034353) glutamate n- acetyltransferase precursor	probable membrane protein YDL247w - yeast (Saccharomyces cerevisiae); (Z74295) ORF YDL247w	GutQ homolog - Escherichia coli	(AL031856) putative involvement in protein glycosylation in the golgi (Schizosaccharomyces nombel	probable hydroxyacylglutathione hydrolase (glyoxalase II) (GLX II); (D83536) unknown [Escherichia coli]; (U70214) hypothetical protein [Escherichia coli]; (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]	(AB011211) pectin methylesterase	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces nombe]	Glycolipid anchored surface protein precursor (glycoprotein GP115); glycophospholipid-anchored surface glycoprotein GAS1 precursor - yeast (Saccharomyces cerevisiae); (X56399) glycoprotein gp115 [Saccharomyces cerevisiae]; (Z49212) Gas1p [Saccharomyces cerevisiae]
% id cvrg 56 34	55	40	63	53		61	42	45
Blast Prob 2.00E-66	6.00E-62 52	4.00E-36 37	1.00E-13 36	1.00E-51 49	0.000000	2.00E-23 37	3.00E-51 58	8.00E-50 47
Blast Score 243	237	105	11	203	59	109	198	197
aat Score 1250	538	366	164	549	43	222	481	1100
ncbi gi g3121733	g3925783	g2119802	g541082	g3738162	g2494853	g4514622	g3560143 481	g1346099 1100 197
Database Hit ncbi gi g31217						•		
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 806-828	580-602	801-828	665-684	197-216 777-796	413-432	524-546	690-714	808-829
Primer 5 pos 23-43	22-43	27-46	22-47	197-216	23-43	49-73	22-49	
Seq num Seq id Contig source 23656 ENU07450 ANI61C5629: 34671943	23657 ENU07451 ANI61C1055: 22-43 871104	23658 ENU07452 ANI61C459:1 27-46 0021	23659 ENU07453 ANI61C9012: 22-47	91	23661 ENU07455 ANI61C1054 5:677283	23662 ENU07456 ANI61C4681: 49-73	23663 ENU07457 ANI61C9019: 22-49 1260397	23664 ENU07458 ANI61C1115: 59-81 13403049

## cina e can e com e

adenosylmethionine-8-amino-7- oxononanoate aminotransferase (7,8- diamino-pelargonic acid aminotransferase) (DAPA aminotransferase); BIO3 protein - yeast (Saccharomyces cerevisiae); (Z71673) ORF YNR058w	lipase - yeast (Geotrichum candidum); (U02387) lipase [Geotrichum candidum]; candidum]; lipase I [Galactomyces	isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase [Fusarium snorotrichioides]	Pyrimidine pathway regulatory protein 1; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae); (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae]; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]	(U24657) saframycin Mx1 synthetase A [Myxococcus xanthus]	transmembrane protein 1; epilepsy holoprosencephaly candidate-1 protein (EHOC-1) (transmembrane protein 1); probable transmembrane protein - human; (U19252) putative transmembrane protein [Homo sapiens]
26		37		10	16
37		3 32	0)	5 25	3 32
6.00E-12	7.00E-1]	1.00E-13	4.00E-12	9.00E-1	3.00E-13 32
89	41	78	72	81	76
125	197	306	89	104	177
g1705462	g1084961	g3915140	g130784	g1171129	g4507551
LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
	794-817	809-828	577-596	805-829	805-823
	13-70	7-54	18-67	14-71	22-41
3666 ENU07460 ANI61C4709: 5321	13667 ENU07461 ANI61C5635: 4 1715495		23669 ENU07463 ANI61C464:4 4 641102	23670 ENU07464 ANI61C464:5 4 8026738	23671 ENU07465 ANIGICI476: 22-41 27621351
	.C4709: LINAP g1705462 125 68 6.00E-12 37 26	43-70 794-817 LINAP g1705462 125 68 6.00E-12 37 26	LINAP g1705462 125 68 6.00E-12 37 26 794-817 LINAP g1084961 197 41 7.00E-11 809-828 LINAP g3915140 306 78 1.00E-13 32 37	LINAP g1705462 125 68 6.00E-12 37 26 794-817 LINAP g1084961 197 41 7.00E-11 809-828 LINAP g3915140 306 78 1.00E-13 32 37 577-596 LINAP g130784 68 72 4.00E-12	LINAP g1705462 125 68 6.00E-12 37 26  794-817 LINAP g1084961 197 41 7.00E-11  809-828 LINAP g3915140 306 78 1.00E-13 32 37  577-596 LINAP g130784 68 72 4.00E-12  805-829 LINAP g1171129 104 81 9.00E-15 25 10

## ota e e e e e e e e e e e

Description (Z68905) ATP-binding cassette multidrug transporter [Emericella	(AL033502) hypothetical membrane protein [Candida albicans]	suppressing protein kinase); dis1- suppressing protein kinase); dis1- fission yeast (Schizosaccharomyces pombe); (D13447) protein kinase Schizosaccharomyces pombel	zinc finger protein SFP1; split zinc finger protein 1 - yeast (Saccharomyces cerevisiae); (U19729) Sfp1p [Saccharomyces cerevisiae]	Galactose-proton symport (galactose transporter); (U28377) ORF_0464 [Escherichia coli]; (AE000377) galactose-proton symport of transport system [Escherichia coli]	(AL022304) putative galactosyltransferase associated protein kinase [Schizosaccharomyces nombe]	probable membrane protein YPL260w - yeast (Saccharomyces cerevisiae); (Z73617) ORF YPL260w [Saccharomyces cerevisiae]	(AL021409) polyketide synthase [Streptomyces coelicolor]	"hypothetical 78.1 KD protein in TIP20-MRF1 intergenic region; hypothetical protein YGL144c - yeast (Saccharomyces cerevisiae); (Z72666) ORF YGL144c [Saccharomyces cerevisiae]; (X99960) putative, YGL144c [Saccharomyces cerevisiae] "
% id cvrg 76 19	92	3	21	54	39	39	7	18
% id 76	38	<del>-</del>	45	53	28	1 45	38	8 4 8
Blast Prob e-119	2.00E-15 38	-300.0	1.00E-33 45	1.00E-19 29	6.00E-51 58	4.00E-20 45	3.00E-25 38	3.00E-25 48
Blast Score 329	82	à	143	91	200	66	115	115
aat Score 3543	154	<u> </u>	328	189	649	318	206	298
ncbi gi g1834342	g3859670	6014171 14171	g417770	g544368	g3006192 649	g2133011	g2808753	g1723926
Database Hit								
Selection Basis LINAP	LINAP	Telepin and the second and the secon	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 804-828		614-637	458-479	806-829	510-536	724-744	426-445	395-414
Primer 5 pos 38-64	i 6	00-83	49-68	30-50	22-49	22-48	38-57	55-74
Seq Prime num Seq id Contig source 5 pos 23672 ENU07466 ANI61C9001: 38-64 33621	23673 ENU07467 ANI61C1476: 51874809	230/4 ENUU/408 ANIOLC3033: 06-83 47484091	23675 ENU07469 ANI61C1115 . 7:54625836	23676 ENU07470 ANI61C9031: 30-50 1938	23677 ENU07471 ANI61C1571: 22-49 6371	23678 ENU07472 ANI61C4717: 22-48 2601027	23679 ENU07473 ANI61C5710: 38-57 17062075	1:5

## ce.ec.cocamono

Description serine/threonine protein kinase STE7; regulatory protein STE7 - yeast (Saccharomyces cerevisiae); (M14097) STE7 protein [Saccharomyces cerevisiae]; (Z67750) regulatory protein STE7 [Saccharomyces cerevisiae]; (Z74207) ORF YDL159w [Saccharomyces cerevisiae]	probable membrane protein YOR320c - yeast (Saccharomyces cerevisiae); (X90565) orf 06145 [Saccharomyces cerevisiae]; (Z75228) ORF YOR320c [Saccharomyces cerevisiae]	(AB014885) HrPOPK-1 [Halocynthia roretzi]	hypothetical 89.2 KD protein in RAR1-SCJ1 intergenic region; probable membrane protein YMR212c - yeast (Saccharomyces cerevisiae); (Z49809) unknown [Saccharomyces cerevisiae]	(AB007927) KIAA0458 protein [Homo sapiens]	"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase); glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae); (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae]; (U30626) glucoamylase [Saccharomyces cerevisiae]; diastaticus] "	glycoprotein GP100 precursor (P29F8); (L04286) glycoprotein gp100 [Dictyostelium discoideum]	(AF059534) severin kinase [Dictyostelium discoideum]
% cvrg	29	30					45
% id 54	35	43					5 37
Blast Prob % 9.00E-37 54	3.00E-17 35	3.00E-46 43	0.07	0.001	0.024	0.0002	2.00E-26 37
Blast Score 152	68	185	38	37	04	45	104
aat Score 320	156	657	175	110	574	71	342
ncbi gi g134968	g2132946 156	g3172111	g2497190	g3413878	g728850	g544411	g3075511
Database Hit ncbi gi g13496							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 358-377	448-467	805-824	803-829	532-551	809-828	285-304	805-824
Primer 5 pos 22-45	22-48	22-47	29-56	22-47	22-43	122-141	22-44
Seq num Seq id Contig source 3 23681 ENU07475 ANI61C1578: 2 1419	23682 ENU07476 ANI61C9003: 22-48 763247	23683 ENU07477 ANI61C1555: 22-47 11288	3784	23685 ENU07479 ANI61C4702: 22-47 16431059	23686 ENU07480 ANI61C9003: 22-43 53067862	23687 ENU07481 ANI61C1598: 122-141 285-304 800.468	23688 ENU07482 ANIGIC1057 8:6031764

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Description (AJ011965) oxidoreductase [Claviceps purpurea] Autophagocytosis protein AUT1;	hypothetical protein YNR007c - yeast (Saccharomyces cerevisiae); (X77395) N2040 [Saccharomyces cerevisiae]; (Z71622) ORF YNR007c [Saccharomyces cerevisiae]	hypothetical 57.3 KD protein GMC- type oxidoreductase CY50.03C; (Z77137) hypothetical protein Rv1279 [Mycobacterium tuberculosis]	probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae); (U51033) Similar in central region to C. elegans hypothetical protein F55C12.5 (GenBank accession number U41107) [Saccharomyces cerevisiae]	(AJ133651) conidiospore surface protein [Trichoderma harzianum] (AB014886) typeII DNA	topoisomerase [Emericella nidulans] (AL033127) hypothetical protein [Schizosaccharomyces pombe]	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase); xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Bacillus pumilus; (X05793) xylan 1,4-beta-xylosidase [Bacillus pumilus]"	(AF030554) class V chitin synthase [Ustilago maydis]	(L40632) ankyrin 3 [Mus musculus]	(D90914) beta-glucosidase [Synechocystis sp.]
% id cvrg 34 30 41 78	2	46	32	17	25	30	54		51
% id 34	:	5 35	3 39	95	) 29	5 46	65	8	1 27
Blast Prob % i 0.000000 34 3 9.00E-21 41		2.00E-26 35	4.00E-53 39	0.046 e-159	8.00E-20 29	2.00E-26 46	e-104	1.00E-13	1.00E-21 27
Blast Score 55		71	208	39 559	86	89	345	78	103
aat Score 131 394			495	183		261	2260	163	200
ncbi gi g4499843 g732206		g1723076	g2133023	g4585623 183 g3172113 174	g3821332	g465491	g2613108	g710551	g1653521
Database Hit ncbi gi g44998									
Selection Basis LINAP		LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 452-479	177-761		743-764	708-728	764-784	452-479	777-795	808-828	786-813
Primer 5 pos 25-48	14-77		22-41	25-44	78-89	22-48	22-47	22-45	54-72
Seq num Seq id Contig source 23689 ENU07483 ANIG1C4702: 36223185		23691 ENU07485 ANI61C1059 4:11061	23692 ENU07486 ANI61C4730: 22-41 9531	23693 ENU07487 ANI61C9036: 25-44 708-728 35942846 23694 ENU07488 ANI61C16:29 122-141 744-763	51437 51437 23695 ENU07489 ANI61C1059 3:11731	23696 ENU07490 ANI61C5643: 22-48 48514395	23697 ENU07491 ANI61C1118 3:53967922	23698 ENU07492 ANI61C57:41 82193	23699 ENU07493 ANIGIC1120 3:44503389

## 

Description hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region; hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae); (Z27116) ORF YKR409 [Saccharomyces cerevisiae]; (Z28314) ORF YKR089c [Saccharomyces cerevisiae]	(M94916) ubiquitin-specific processing protease [Saccharomyces cerevisiae]	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase); (X95584) 1- pyrroline-5-carboxylate dehydrogenase [Agaricus bisporus]	(AF107264) glutamate synthase large subunit [Rhizobium etli]	Metal homeostatis protein BSD2; metal homeostasis protein BSD2 -	yeast (Saccharomyces cerevisiae); (X76053) YBR2037-ORF [Saccharomyces cerevisiae]; (L33783) metal homeostasis protein	[Saccharomyces cerevisiae]; (Z36159) ORF YBR290w [Saccharomyces cerevisiae]; ORF YBR2037 [Saccharomyces cerevisiae]	(AL035247) ion transporter [Schizosaccharomyces pombe]	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]	hypothetical 47.8 KD protein in HSP26-TJF32 intergenic region; aminopeptidase Y homolog - yeast (Saccharomyces cerevisiae); (X76294) ORF YBRO718 [Saccharomyces cerevisiae]; (Z35943) ORF YBR074w [Saccharomyces cerevisiae]
% id cvrg 43 29		46	7				59	13	43
% id		48	45				5 41	33	41
Blast Prob % i 1.00E-49 43	1.00E-27	7.00E-57 48	1.00E-14 45	2.00E-15			9.00E-26 41	5.00E-21 39	6.00E-22 41
Blast Score 161	123	150	53	72			117	101	66
aat Score 775	510	558	230	172			644	316	187
ncbi gi g549643	g173128	g2494072	g4038458	g586358			g4164420 644	g85105	g586511
Database Hit ncbi gi g54964									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP			LINAP	LINAP	LINAP
Primer 3 pos 807-829	804-829	730-754	367-387	453-479			889-899	749-773	419-438
Primer 5 pos 22-43	22-49	40-59	36-55	64-83			29-47	34-53	22-49
Seq num Seq id Contig source 23700 ENU07494 ANI61C1059 8:2380882	23701 ENU07495 ANI61C465:2 22-49 4784468	23702 ENU07496 ANI61C5689: 40-59 38974786	23703 ENU07497 ANI61C1060 0:22132711	23704 ENU07498 ANI61C465:9 64-83 1209481			23705 ENU07499 ANI61C1058 6:20541345	23706 ENU07500 ANI61C4751: 34-53 8711704	23707 ENU07501 ANI61C6475: 22-49 14532048
Seq id ENU07494	ENU07495	ENU07496	ENU07497	ENU07498			ENU07499	ENU07500	ENU07501
Seq num 23700	23701	23702	23703	23704			23705	23706	23707

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	EMBL:D/34/b come GLT1 protein - yeast (Saccharomyces cerevisiae); (Z67750) putative protein [Saccharomyces cerevisiae]; (Z74219) ORF YDL171c [Saccharomyces	(L35601) ankyrin [Drosophila melanogaster]; ankyrin [Drosophila	(AL031540) hypothetical ATP binding	"sodium channel protein, skeletal muscle alpha-subunit (MU-1); sodium channel protein mul alpha chain, skeletal muscle - rat; (M26643) voltage-sensitive sodium channel alpha	subunit [Rattus norvegicus]" putative 89.3 KD transcriptional regulatory protein C1F7.11C; hypothetical protein SPAC1F7.11c - fission yeast (Schizosaccharomyces pombe); (Z67998) unknown	[Schizosaccharomyces pombe] (AF015825) malate dehydrogenase-like protein [Bacillus subtilis]; (Z99110) similar to malate dehydrogenase	(AB015306) Leukotriene B4 omega-	(AL031035) putative ATP/GTP-binding protein [Streptomyces coelicolor]
cvrg 100	Ξ		21		16	62	31	13
Blast Prob % id 0.000003 39	1.00E-77 65	0.000000	1.00E-25 43	0.35	3.00E-10 28	2.00E-23 35	4.00E-18 34	0.000000 33 05
Blast Score 52	196	55	116	36	9	109	91	28
aat Score 95	873	38	366	720	106	322	217	49
ncbi gi g3879015	g2131263	g557084	g3581879	g116453	g1351672 106	g2612904	g4519535	g3319757
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 457-476	725-746	456-479	595-620	802-829	386-413	803-829	459-478	456-479
Seq Primer num Seq id Contig source 5 pos 23708 ENU07502 ANI61C9037: 22-45 17531442	23709 ENU07503 ANI61C1611: 46-65 1330376	23710 ENU07504 ANI61C6464: 36-54 666332	23711 ENU07505 ANI61C9056: 97-116 595-620	23712 ENU07506 ANI61C1557: 22-47 44032640	23713 ENU07507 ANI61C5732: 22-46 5161	23714 ENU07508 ANI61C6469: 41-60 1051174	23715 ENU07509 ANIGIC1619: 48-69	23716 ENU07510 ANI61C567:1 32-51 213866

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Description (AP000004) 275aa long hypothetical translation initiation factor eIF-2 alpha	positive regulator of purine utilisation; positive regulator of purine utilisation : Emericella nidulans; (X84015) positive regulator of purine utilisation	morphogenesis-related protein (multicopy suppression of a budding defect 1); morphogenesis-related protein MSB1 - yeast (Saccharomyces cerevisiae); (M37767) multicopy suppressor of a budding defect [Saccharomyces cerevisiae]; (Z5096) ORF YOR 188w [Saccharomyces	cerevisiae] (AF045014) translation release factor	ekr's [rodospora ansenna] (Z68905) ATP-binding cassette multidrug transporter [Emericella	ATP-dependent protease LA; (AF030688) ATP-dependent proteinase	[Mycobacterium sineginaus] (AF052482) germinating protein	Letysipue graninus) Leserine dehydratase (Leserine deaminase); Leserine dehydratase (EC 4.2.1.13) SDL1 - yeast (Saccharomyces cerevisiae); (X52657) Leserine dehydratase (AA 1-338)	[Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps	purpureaj internalin B - Listeria monocytogenes
% id cvrg	15	18	38	10	14	91	78	40	
pi %	28	30	69	99 ,	29	45	45	42	
Blast Prob 0.08	3.00E-13 28	4.00E-11 30	e-101	4.00E-37 66	0.00001 29	6.00E-29 45	1.00E-35 42	2.00E-15 42	0.00002
Blast Score 37	75	8	356	154	20	127	91	83	49
aat Score 91	48	149	1046	439	57	299	373	270	28
ncbi gi g3257375	g1351343	g127338	g2832315	g1834342	g3913990	g2981452	g134388	g4499843	989868
Database Hit									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 443-470	458-477	670-695		457-479		502-528	804-829	646-665	331-350
Seq Primer num Seq id Contig source 5 pos 23717 ENU07511 ANI61C6430: 30-51 66536314	23718 ENU07512 ANI61C9058: 57-76 1509	23719 ENU07513 ANI61C568:2 22-48 8803595	23720 ENU07514 ANI61C9070:	11181 23721 ENU07515 ANGIC1617: 25-52 15832072	23722 ENU07516 ANI61C4767: 102-127 453-479 3181	23723 ENU07517 ANI61C568:7 28-47	23724 ENU07518 ANI61C6462: 70-89 41853107	23725 ENU07519 ANIGIC9042: 22-41	1623912 23726 ENU07520 ANI61C1628: 25-50 24532797

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Description "(Z81586) predicted using Genefinder; similar to Alcohol/other dehydrogenases, short chain type	(Z71177) Similarity with human nuclear autoantigen (PIR accession number JC2522); cDNA EST EMBL:D65093 comes from this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk353f10; (Z71181) Similarity with human nuclear autoantigen (PIR accession number JC2522); cDNA EST EMBL:D65093 comes from this gene; cDNA EST grom this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk297d9.5	(Z99532) putative integral membrane	hypothetical 30.0 KD protein C18G6.01C in chromosome I; (Z68198) hypothetical protein	Thermostable beta-glucosidase B (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase); beta-glucosidase (EC 3.2.1.21) B - Clostridium thermocellum; (X15644) bglB gene (AA1-754) [Clostridium thermocellum]	(L40632) ankyrin 3 [Mus musculus]	(U68040) polyketide synthase [Cochliobolus heterostrophus]
% id cvrg		36	71	52	9	8
		2 51	0 34	1 40	3 40	3 40
Blast Prob 2.00E-14	1.00E-12	3.00E-72 51	0.000000 34	6.00E-21 40	2.00E-13	2.00E-13 40
	<u> </u>		ö ö	9	2.	2.
Blast Score 59	73	272	61	87	75	52
aat Score 99	112	1023	102	220	126	248
ncbi gi g3924850	g3873652	g2440206 1023	g1351719 102	g114959	g710552	g1546072
Database Hit ncbi gi g39248						
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 611-629	451-470	721-740	685-709		346-365	444-463
Primer 5 pos 24-51	14-81	1-50	12-49		22-46	22-48
	780: 5	751: 3	462: 2	042: 8	062 2	785: 2
Contig source ANI61C1060 4:19871325	ANI61C4 94516	ANI61C5	ANI61C64 52225951	ANI61C90 58925338	ANI61C1	ANI61C4 7641211
Seq num Seq id Contig source 23727 ENU07521 ANI61C1060 4:19871325	23728 ENU07522 ANI61C4780: 54-81 94516	23729 ENU07523 ANI61C5751: 31-50	23730 ENU07524 ANI61C6462: 22-49 52225951	23731 ENU07525 ANI61C9042: 58925338	23732 ENU07526 ANI61C1062	23733 ENU07527 ANI61C4785: 22-48 7641211
Seq id ENU0752	U075.	TU0752	TU075;	TU075.	TU075;	TU075:
Sec 27 EN	28 EN	29 EN	30 EN	31 EN	32 EN	33 EN
Seq num 2372	237.	237.	237.	237.	237.	237.

## ngungen nepr

Description Probable membrane protein YOL002c -	yeast (Saccharomyces cerevisiae); (U43491) hypothetical protein UND327 [Saccharomyces cerevisiae]; (Z74744) ORF YOL002c [Saccharomyces cerevisiae]		probable glucoSE transporter HXT5; hexose transport protein HXT5 - yeast (Saccharomyces cerevisiae); (X77961) hexose transporter [Saccharomyces cerevisiae]; (U00060) Hxt5n; Hexose	transporter [Saccharomyces cerevisiae]	A-agglutinin attachment subunit precursor; a-agglutinin core protein	AGA1 - yeast (Saccharomyces	cerevisiae); (MoO390) a-aggiuunin core subunit [Saccharomyces	cerevisiae]; (Z71659) ORF YNR044w	(AF009417) cytochrome P450	[Myrothecium roridum]	(Z97052) hypothetical protein [Schizosaccharomyces pombe]	hypothetical protein MJ0301;	Methanococcus jannaschii; (U67485)	conserved hypothetical protein [Methanococcus iannaschii]	(L35053) endonuclease [Magnaporthe grisea]	general alpha-glucoside permease; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae); (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
% % id cvrg 38 53									39	i	52	34			23	
% ic 38		29	0						3 39	!	3 40	1 32			6 44	4
Blast Prob %			0.000000		0.003				2.00E-23 39		2.00E-43 40	2.00E-11 32			2.00E-56 44	2.00E-14
Blast Score 130			45		42				109		176	69			219	80
aat Score 256		30	159		101				474	;	682	124			755	74
ncbi gi e2132816	o c		g729781		g416592				g2267601		g2213557	g2495901 124			g522302	g1703215
Database Hit ncbi gi																
Selection Basis LINAP		LINAP	LINAP		LINAP				LINAP		LINAP	LINAP			LINAP	LINAP
Primer 3 pos 422-448					452-479				807-829		720-741	450-477			673-700	789-808
Primer 5 pos					32-108				12-21		57-74	40-62			179-206	37-56
Seq Prime num Seq id Contig source 5 pos 23734 ENII07528 ANI61C6502: 22-47	240779	23735 ENU07529 ANI61C4789: 10931483	23736 ENU07530 ANI61C5728: 11821849		23737 ENU07531 ANI61C6472: 82-108 452-479 25822106				23738 ENU07532 ANI61C907:8 45-71	21854	23739 ENU07533 ANI61C1652: 57-74 12492315	_	3.41303628		23741 ENU07535 ANI61C5782: 179-206 673-700 11467	23742 ENU07536 ANI61C6429: 37-56 44042930

## cocanos comunicados

	Description hypothetical 33.3 KD protein in PERR-ARGF intergenic region; (AE000134) putative lyase/synthase [Escherichia coli]	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region; probable membrane protein YGR010w - yeast (Saccharomyces cerevisiae); (Z72795) ORF YGR010w [Saccharomyces cerevisiae]	(AJ010902) inversin [Mus musculus]	(Y13568) beta-xylosidase [Emericella nidulans]	(AB007924) KIAA0455 protein [Homo sapiens]	probable membrane protein YLR242c - yeast (Saccharomyces cerevisiae); (U20865) Arv1p [Saccharomyces cerevisiae]	conidial green pigment synthase; probable polyketide synthase - Emericella nidulans; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans]; wA gene [Emericella nidulans]	hypothetical 11.5 KD protein in HTB2-NTH2 intergenic region; hypothetical protein YBL001c - yeast (Saccharomyces cerevisiae); (Z26494) unknown [Saccharomyces cerevisiae]; (Z35762) ORF YBL001c [Saccharomyces cerevisiae] YBL0105 [Saccharomyces cerevisiae]
%	% id cvrg 27 86	37	26	28			41	
Blast	Prob 6.00E-15	7.00E-37 52	2.00E-11 25	3.00E-63 51	1.6	5.3	1.00E-53 37	0.14
	Score 82	153	70	242	33	32	210	36
aat	Score 174	355	148	498	891	84	547	166
	ncbi gi g2494090	g1723643 355	g3757672 148	g2920706 498	g3413872 168	g1363735	g549443	g465533
	Database Hit ncbi gi g2494(							
Selection	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 757-776	431-454	774-797	558-576	438-457	796-823	806-829	458-479
Primer	5 pos 26-47	47-66	22-49	104-125	71-90	106-133	32-52	22-48
	Contig source ANI61C9091: 1571756	ANI61C1675: 17392203	ANI61C1061 4:20633065	ANI61C4814: 6941	ANI61C4817: 1225914	ANI61C566:6 8607865	ANIGIC4815: 1691415	
Seq	num Seq id Contig source 5 pos 23743 ENU07537 ANI61C9091: 26-47 1571756	23744 ENU07538 ANI61C1675: 47-66 17392203	23745 ENU07539 ANI61C1061 4:20633065	23746 ENU07540 ANI61C4814: 104-125 558-576 6941	23747 ENU07541 ANI61C4817: 71-90 1225914	23748 ENU07542 ANI61C566:6 106-133 796-823 8607865	23749 ENU07543 ANI61C4815: 32-52 1691415	23750 ENU07544 ANI61C1062 2:49905304

## odecan'i ashino

	[Homo sapiens] NF-180 - sea lamprey; (U19361) NF- 180 [Petromyzon marinus] probable membrane protein YPL006w - yeast (Saccharomyces cerevisiae); (Z48483) unknown [Saccharomyces cerevisiae]; (U33335) Lpa11p [Saccharomyces cerevisiae]; (Z71255)	unknown [Saccharomyces cerevisiae] MLO2 protein; (L42550) ORF [Schizosaccharomyces pombe] (U62774) cytochrome P450 monooxygenase [Aspergillus parasiticus] (AL023594) amino-acid permease	l'Schizosaccharonyces pomoej "(D86544) hydroxyquinol-1, 2- dioxygenase [Ralstonia pickettii] " (M15991) tRNA isopentenyl transferase [Saccharomyces cerevisiae] (U68040) polyketide synthase [Cochliobolus heterostrophus]	putative dioxygenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae] (AJ222967) cystinosin [Homo sapiens]; (Y15924) cystinosin [Homo sapiens]
% id cvrg 38 25	23	30	80 53 10	35
% id 5 38	2 39	2 53 5 37 0 32	4 33 9 41 2 41	0 30
Blast Prob % 6.00E-35 38	0.053 6.00E-42 39	2.00E-32 53 2.00E-16 37 2.00E-10 32	2.00E-34 33 4.00E-39 41 3.00E-22 41	0.000000 30 4 3.00E-22 39
Blast Score 148	39 · 171	85	106 162 63	55
aat Score 421	837	280 95 108	315 293 394	378
ncbi gi g4505499	g2133786 g1077259	g2498563 g2689471 g3150139	g1437475 g171963 g1546072	g2497056
Database Hit ncbi gi g45054				
Selection Basis LINAP	LINAP	LINAP LINAP LINAP	LINAP LINAP LINAP	LINAP
Primer 3 pos 712-738	779-806	529-548	793-817 795-814 809-828	635-656
Primer 5 pos 46-72	22-44	25-48	28-47 59-78 40-59	26-45
Seq Prime num Seq id Contig source 5 pos 23751 ENU07545 ANI61C9597: 46-72 8481	23752 ENU07546 ANI61C9593: 22-44 22133056 23753 ENU07547 ANI61C6503: 57-76 2076449	23754 ENU07548 ANIGICI674: 22-48 892300 23755 ENU07549 ANIGIC9034: 25-52 49995519 23756 ENU07550 ANIGIC650:2	0802671 23757 ENU07551 ANI61C909:4 28-47 711308 23758 ENU07552 ANI61C9556: 59-78 11621997 23759 ENU07553 ANI61C5675: 40-59 61494744	23760 ENU07554 ANI61C1122 26-45 8:61036779 8:3761 ENU07555 ANI61C9102: 22-42

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Description hypothetical 44.5 KD protein in PDE1- RTF1 intergenic region; hypothetical protein YGL246c - yeast (Saccharomyces cerevisiae); (X94357) ORF NRE387 [Saccharomyces cerevisiae]; (Z72768) ORF YGL246c [Saccharomyces cerevisiae]	(AL023587) putative kinesin-like protein [Schizosaccharomyces pombe] quinate permease (quinate transporter); quinate transport protein - Emericella nidulans; (X13525) quinate permease Emericella nidulans	"probable calcium-transporting ATPase (adopplasmic reticulum CA2+-ATPase); probable ATPase (EC 3.6.1) DRS2 - yeast (Saccharomyces cerevisiae); (L01795) ATPase (Saccharomyces cerevisiae]; (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase (Saccharomyces cerevisiae] "	Start control protein CDC10; cdc10 start control protein - fission yeast (Schizosaccharomyces pombe); (X02175) cdc10 polypeptide [Schizosaccharomyces pombe]	(U78597) kinesin light chain [Plectonema boryanum]	(ALU31/98) putative leucine permease transcriptional regulator. [Schizosaccharomyces pombe]	[Homo sapiens] (AF102265) N-acetylglucosamine- phosphate mutase [Homo sapiens]
% 1 cvrg 53	26	٢	34	45	3 %	32
Blast Prob % id 6.00E-13 32	2.00E-48 54 4.00E-29	7.00E-33 63	3.00E-31 35	6.00E-16 29	7.00E-38 40 2.106 69	.26
Blast Score 59	168	140	135	85	157	119
aat Score 296	381	304	375	225	402	
ncbi gi g1723981	g3136023 g131768	g728905	g115906	g2645229	g3687460 402	g3851711
Database Hit ncbi gi g17239						
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 694-721	627-651	439-466	805-823	610-637	808-829	546-573
Primer 5 pos 23-47	22-49	25-44	9-85	29-51	22-47	33-52 22-47
Seq num Seq id Contig source : 23762 ENU07556 ANI61C9556: 38683127	23763 ENU07557 ANI61C6476: 22-49 45715242 23764 ENU07558 ANI61C1685: 22-47 2981945	23765 ENU07559 ANI61C1127 25-44 6:342642	23766 ENU07560 ANI61C5756: 66-85 20563660	23767 ENU07561 ANI61C1127 29-51 1:6691	23768 ENU07562 ANI61C9579: 22-47 67515631	23/09 ENU0/303 ANIOLCO3:33 33-52 114969 23770 ENU07564 ANIOLC5811: 22-47 6461

## ota e e cara camana e

Description quinate transporter); quinate transporter); quinate transport protein - Emericella nidulans; (X13525) quinate permease (Emericella nidulans)	Spliceosome associated protein 49 (SAP 49) (SF3B53); spliceosomeassociated protein SAP-49 - human; (L35013) spliceosomal protein [Homosaniens]	probable membrane protein YOR034c-yeast (Saccharomyces cerevisiae); (X87331) AKR1 homologue; overlaps with L31407 [Saccharomyces cerevisiae]; (Z74942) ORF YOR034c [Saccharomyces cerevisiae]	(AJ223459) PmA protein [Emericella nidulans]	hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae); (Z74957) ORF YOR049c [Saccharomyces cerevisiae]	alpha-glucosidase precursor (maltase); alpha-glucosidase (EC 3.2.1.20) - barley; (U22450) alpha-glucosidase [Hordeum vulgare]	"Immunoglobulin G binding protein H precursor (protein H); protein H precursor - Streptococcus sp. (group A, strain 40/58); (M29398) protein H precursor [Streptococcus sp.]"	(U24215) HOMODA hydrolase [Pseudomonas putida]; HOMODA hydrolase [Pseudomonas putida]	multiDRUG resistance protein 2 (P-glycoprotein 2); multidrug resistance protein 2 - mouse; (J03398) multidrug resistance protein [Mus musculus]
% cvrg	51				27		46	12
% id	47		0	_	41		26	48
Blast Prob % 6.00E-10 31	4.00E-30 47	0.000000	0.000000	1.00E-24	1.00E-42 41	0.095	0.0002	3.00E-33 48
Blast Score 61	100	28	55	901	107	37	46	139
aat Score 87	621	170	42	104	926	65	72	745
ncbi gi g131768	g2500587	g2132865	g2808662 42	g2132036 104	g3023275	g1711494	g1263187	g126929
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 439-458	767-786	506-525	455-479	810-829	810-829	526-548	458-479	726-749
Primer 5 pos 52-74	22-48	38-57	22-43	22-44	22-48	22-45	23-45	22-45
Seq Pontig Source 5 23771 ENU07565 ANI61C1123 5 1:3381	23772 ENU07566 ANI61C5803: 22-48 3121387	23773 ENU07567 ANI61C1703: 38-57 1542994	23774 ENU07568 ANI61C1123 2 1:20541750	23775 ENU07569 ANI61C9063: 2 85567615	23776 ENU07570 ANI61C4823: 22-48 49283780	23777 ENU07571 ANI61C9110: 22-45 18741306	23778 ENU07572 ANI61C9578: 23-45 45224933	23779 ENU07573 ANI61C4906: 22-45 22681

## oceniu ocenu

	Description (Z98056) putative glyxoxylate pathway regulator [Schizosaccharomyces pombe]	U58946) transposase [Aspergillus awamori]	(AL035254) putative transcriptional regulator [Schizosaccharomyces pombe]	Ferric reductase transmembrane component 7 precursor; probable membrane protein YOL152w - yeast	(Saccharomyces cerevisiae); (Z48239) orf1 [Saccharomyces cerevisiae]; (Z74894) ORF YOL152w	[Saccharomyces cerevisiae] (AJ131720) alpha integrin binding	protein 80 [Homo sapiens] (M80674) hydroxylase [Streptomyces	grancescens) (Z83857) ppsC [Mycobacterium tuberculosis]	"hypothetical 43.0 KD protein in cute-GLNX intergenic region; (AE000170) orf, hypothetical protein [Escherichia	Conj., (D20700) VISC protein [Escherichia coli] " (AJ133272) atrophin-1 [Pongo pvemaeus]	CZ4030) predicted using Genefinder; cDNA EST EMBL:C07609 comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com
%	% id cvrg	51	20	42		14	14	=			65
Blast	Prob 0.000006	1.00E-92 55	0.000000 28 2	2.00E-33 32		1.00E-19 41	9.00E-10 49	6.00E-45 39	0.0003	1.8	8.00E-40 42
Blast	Score 50	339	56	143		95	63	181	46	34	164
aat	Score 117	914	82	405		210	143	494	82	127	370
	ncbi gi g2281979	g1805251	g4165298	g3913676 405		g4468913	g769829	g3242253	g3025210	g4467980	g3875304
	Database Hit ncbi gi g22819										
Selection	Basis LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	3 pos 312-332	807-826	455-479	787-806		297-319	319-346	803-829	398-420	714-741	651-670
Primer	5 pos 114-133	22-47	22-45	23-43		22-48	102-123	23-46	53-72	32-51	32-51
	num Seq id Contig source 5 pos 3 pos 23780 ENU07574 ANI61C1715: 114-133 312-332 1354	23781 ENU07575 ANI61C9108: 22-47 37442763	23782 ENU07576 ANI61C5784: 22-45 35923988	23783 ENU07577 ANI61C4909: 23-43 13292684			5:15241185 23785 ENU07579 ANI61C1709: 102-123 319-346	23786 ENU07580 ANI61C5854: 23-46 11173	23787 ENU07581 ANI61C1127 53-72 8:6071	23788 ENU07582 ANI61C4930: 32-51	23789 ENU07583 ANIGIC1127: 32-51 24533163

## recentoro

	hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae); (X99000) ORF D1075 [Saccharomyces cerevisiae]; (Z74249) ORF YDL201w	hypothetical 42.2 KD protein C17G8.11C in chromosome I; (Z69795) unknown	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease	(Z98533) phosphoribosylformylglycinamidine synthase [Schizosaccharomyces	pombel (AL033388) rrm3-pif1 helicase homolog [Schizosaccharomyces	pomoe) (AL033388) putative calcium- transporting atpase	[Schizosaccharomyces pombe] (AF119122) serotonin transporter [Bos taurus]
% id cvrg 47 23	99	38	84	20	32	22	4
% id	58	27	39	2	52	8 63	29
Blast Prob % 1 4.00E-40 47	1.00E-40 58	4.00E-11 27	3.00E-45 39	4.00E-69 64	1.00E-71 52	8.00E-98 63	7.00E-29 29
Blast Score 165	166	89	124	260	185	356	75
aat Score 602	535	97	574	1810	948	3130	353
ncbi gi g548585	g2131358	g1723483	g125935	g2330857	g3850110	g3850108	g4588918
Database Hit ncbi gi g54858							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 807-829	806-825	456-479	800-822	727-746	726-745	806-828	796-815
Primer 5 pos 32-51	23-43	22-45	24-43	22-45	22-45	23-50	22-42
Seq Prime num Seq id Contig source 5 pos 23790 ENU07584 ANI61C9603: 32-51 13112844	23791 ENU07585 ANI61C6528: 23-43 22661157	23792 ENU07586 ANI61C9619: 22-45 91512	23793 ENU07587 ANI61C6539: 24-43 11262	23794 ENU07588 ANI61C5850: 22-45 15593577	23795 ENU07589 ANI61C1130 22-45 0:12451	23796 ENU07590 ANI61C9114: 23-50 13099	23797 ENU07591 ANI61C6538: 22-42 15912558

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Description Pyrimidine pathway regulatory protein 1; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae); (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae]; (Z73186) ORF YLR014c [Saccharomyces	(M57453) sterol carrier protein-x [Rattus norvegicus] transaldolase; (D90900) transaldolase [Synechocystis sn.]	probable sucrose utilization protein SUC1 (Z98529) putative cytoskeleton assembly control protein	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) - Penicillium griscofulvum; (M37461) EA \$2 protein [Penicillium patulum]"	(U43200) antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]	(AJ010902) inversin [Mus musculus]	hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region; hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae); (Z27116) ORF YKR409 [Saccharomyces cerevisiae]; (Z28314) ORF YKR089c [Saccharomyces cerevisiae]	probable calcium-transporting ATPase 4; probable ATPase (EC 3.6.1) YDR093w - yeast (Saccharomyces cerevisiae); (Z47746) probable ATPase [Saccharomyces cerevisiae]
% cvrg	33	47	15	53			17
% id %	52	35	44	26			, 55
Blast Prob % 8.00E-13 25	4.00E-65 52 0.000000 34	0.000000 28 02 1.00E-34 35	2.00E-52 44	0.61	5.00E-28	0.000000	9.00E-87 55
Blast Score 74	177	60	185	35	125	41	320
aat Score 126	086	181	1655	129	248	284	1141
ncbi gi g130784	g206877 g2501349	g1174472 181 g2330690 481	g119830		g3757672	g549643	g2493010 1141
Database Hit ncbi gi g13078							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 376-399	788-807	809-828	728-748	808-827	807-829	102-129 705-729	622-649
5 pos 26-53	22-47	22-47	26-53	47-67	24-47	102-129	22-49
Seq id Contig source ENU07592 ANI61C1131 4:6891089	23799 ENU07593 ANIGICI711: 22-47 51373884 23800 ENU07594 ANIGIC9114: 22-49	t5: 34:	23803 ENU07597 ANI61C1119: 26-53 924411350	23804 ENU07598 ANI61C9134: 47-67 14392299	23805 ENU07599 ANI61C9625: 24-47 4431412	23806 ENU07600 ANI61C1131 8:24811732	23807 ENU07601 ANI61C1721: 22-49 8002490
Seq num 23798	23799	23801	23803	23804	23805	23806	23807

Description (AL031535) RNA binding protein	[Schizosaccharomyces pombe] (AL021748) adenosine deaminase	[Schizosaccharomyces pombe] (AC004684) hypothetical protein [Arabidopsis thaliana]	Azzel ; finger protein AZF1, asparagine-rich zotein AZF1, asparagine-rich - yeast (Saccharomyces cerevisiae) ; (Z26253) zinc finger protein of 101170 Da [Saccharomyces cerevisiae] ; (X90518) ORF 03244	YOR3244w [Saccharomyces cerevisiae]; (A74333) YOR3244w [Saccharomyces cerevisiae]; (Z75021) ORF YOR113w [Saccharomyces cerevisiae] "	(M61773) ATP12 [Saccharomyces cerevisiae]	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans]; (U39847) AO66 ankyrin	Cachornagonus eregans) (AL031263) putative GTPase-activator protein for Rho-like GTPases (Schizosaccharomyces pombe)	"citrate synthase, mitochondrial precursor; (D63376) citrate synthase precursor [Aspergillus niger] "	(AC006841) putative pol protein with Zn finger CCHC type domain [Arabidopsis thaliana]	plasma membrane Ca2+-ATPase isoform 4 - rat; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus]
% cvrg 29	46	48		9	83	<b>∞</b>	73	48	11	15
% id 48	42	36		à	97	30	36	88	34	43
Blast Prob %	3.00E-24 42	0.000000 36	2.00E-41		9.00E-21 26	9.00E-12 30	5.00E-10 36	e-104	0.00002	1.00E-31 43
Blast Score	112	59	66	Š	101	70	65	335	49	112
aat Score 328	191	140	379		261	87	227	1276	104	323
ncbi gi g3560261	g2842505	g3236250	g1168610 379		g1/1106	g1208874	g3417437	g1705871	g4567277	g1083757
Database Hit ncbi gi										
Selection Basis LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 451-472	633-656	709-730	639-661		792-815	452-479		699-721	446-465	448-467
Seq Primer num Seq id Contig source 5 pos 23808 EN107602 ANI61C9117: 23.44		258934 23810 ENU07604 ANI61C6489: 48-67 48924135	23811 ENU07605 ANIGIC5883: 23-42 30202339			23813 ENU07607 ANI61C6547: 22-46 493988	23814 ENU07608 ANI61C1132 6:15902375	23815 ENU07609 ANI61C1735: 22-43 1650417	23816 ENU07610 ANI61C1745: 34-59 31332756	23817 ENU07611 ANI61C5888: 156-183 448-467 40573501

Description hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae); (Z35912) ORF YBR043c [Saccharomyces	(AL035263) homoserine dehydrogenase [Schizosaccharomyces pombe]	(AL023705) hypothetical protein [Schizosaccharomyces pombe]	(AB004537) methionyl-tRNA synthetase [Schizosaccharomyces	ponnoel (U07187) Mih1p [Saccharomyces cerevisiae]	(M33703) Hex2 protein [Saccharomyces cerevisiae]	(Z98979) putative phosphatidylserine decarboxylase proenzyme	UV radiation resistance associated gene; (X99050) p63 (processed form) [Homo sapiens]	(U29156) involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author. [Mus musculus]	(AF000975) 7-O-methyltransferase [Medicago sativa]	probable membrane protein YOR019w - yeast (Saccharomyces cerevisiae); (X87331) ORF OR26.09 [Saccharomyces cerevisiae]; (Z74927) ORF YOR019w [Saccharomyces	cerevisiae] (U49439) ASH1 [Drosophila melanogaster]
% cvrg 23	55	48		20	10	16	43	30			10
% id 29	51	34	_	43	47	) 26	. 27	5 29			33
Blast Prob 0.00005	1.00E-56 51	2.00E-18 34	0.000000	3.00E-28 43	2.00E-21 47	0.000000 26 002	4.00E-23 27	7.00E-28 29	4.00E-10	4	3.00E-19 33
Blast Score 48	219	92	52	125	94	62	108	124	65	32	79
aat Score 99	524	115	54	231	185	107	260	309	95	101	212
ncbi gi g586486	g4176520	g3169083	g2257528	g460627	g171666	g2388966	g4507861	g968973	g2580582	g1078035	g1335892
Database Hit ncbi gi g58648											
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 451-478	566-585	452-479	309-328	376-399	422-441	432-451	802-829	781-800	455-475	800-819	694-713
Primer 5 pos 22-45	27-45	22-49	50-70	30-57	28-77	62-09	22-47	22-43	35-55	30-53	102-120
Seq num Seq id Contig source 23818 ENU07612 ANI61C1135 3:746396	23819 ENU07613 ANI61C2700: 27-45 6391	23820 ENU07614 ANI61C6547: 22-49	23821 ENU07615 ANIGIC9647: 50-70 1368	23822 ENU07616 ANI61C658:3 30-57	23823 ENU07617 ANI61C1736: 58-77	23824 ENU07618 ANIGIC2666: 60-79 3611	23825 ENU07619 ANI61C9142: 22-47 4521659	23826 ENU07620 ANI61C9630: 22-43 43712964	23827 ENU07621 ANI61C6496: 35-55 6254_5908	23828 ENU07622 ANIGICS884: 30-53 23691036	23829 ENU07623 ANI61C9145: 102-120 694-713 1814

Description positive regulator of purine utilisation; positive regulator of purine utilisation - Emericella nidulans; (X84015) positive regulator of purine utilisation [Emericella nidulans]	(Z82044) hypothetical 54.4 kd protein [Bacillus subtilis]	(AB014596) KIAA0696 protein [Homo sapiens]	ANKYRIN; ankyrin - mouse; (M84756) ankyrin [Mus musculus]	(U46069) fertilin alpha subunit [Oryctolagus cuniculus]	Pyrimidine pathway regulatory protein 1; regulatory protein PPR1 - yeast	(Saccharomyces cerevisiae); (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae]; (Z73186)	ORF 1 LK014c [Saccharomyces cerevisiae]	(Z74697) ppsA [Mycobacterium tuberculosis]	(AL023777) hypothetical protein [Schizosaccharomyces pombe]	(U43720) Sug2p [Saccharomyces cerevisiae]	(AC000098) EST gb ATTS1136 comes from this gene. [Arabidopsis thaliana]	hypothetical 44.9 KD protein C18B11.02C in chromosome I; hypothetical protein SPAC18B11.02c - fission yeast (Schizosaccharomyces pombe); (Z50728) hypothetical protein [Schizosaccharomyces pombe]
% % id cvrg 30 11		41	∞		18			13	32	27		63
% id 30		39	35	_	31			41	37	78		20
Blast Blast Score Prob 36 0.23	3.00E-10	9.00E-36 39	2.00E-16 35	0.000000	8.00E-13 31			6.00E-43 41	7.00E-29 37	e-101	0.046	5.00E-66 50
	65	150	82	55	74			146	127	254	38	251
aat Score 103	145	300	101	78	79			579	185	1005	69	773
143	g1673402 145	g3327206 300	g1168457	g1245061	g130784			g3261605 579	g3184102 185	g1147800 1005	g2388584 69	g1175381 773
Database Hit ncbi gi g13512												
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP			LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 452-479	452-479	806-828	375-394	99-119	422-442			805-827	568-590	803-829	458-479	808-827
Primer 5 pos 35-55	24-43	47-74	27-46	22-49	55-74			22-45	22-45	65-91	22-46	22-49
Seq num Seq id Contig source 5 pos 23830 ENU07624 ANI61C9601: 35-55 9301297	23831 ENU07625 ANI61C6553: 24-43	23832 ENU07626 ANI61C1734: 47-74 55544663	23833 ENU07627 ANI61C2767: 27-46 6511125	23834 ENU07628 ANI61C9145: 22-49	23835 ENU07629 ANI61C9601: 55-74			23836 ENU07630 ANI61C1131: 22-45 28841508	23837 ENU07631 ANI61C1757: 22-45 18672501	23838 ENU07632 ANI61C2764: 65-91 1339358	23839 ENU07633 ANI61C9144: 22-46 20942560	23840 ENU07634 ANI61C6543: 22-49 6591663

Description CBP3 protein precursor; membrane protein CBP3 - yeast (Saccharomyces cerevisiae); (J04830) CBP3 protein [Saccharomyces cerevisiae]; (Z73571) ORF YPL215w [Saccharomyces cerevisiae] (X97001) LR8B [Gallus gallus]	Pectate lyase L precursor; (L42248)	"(AC002292) similar to ""Mx"" GTP-binding proteins [Arabidopsis thaliana]	hypothetical 70.6 KD protein in PGD1-STT3 intergenic region; hypothetical protein YGL023c - yeast (Saccharomyces cerevisiae); (Z72545) ORF YGL023c [Saccharomyces	"(AL021837) SPBC947.05c, ferric reductase transmembrane component, (possibility of intron between 15640-15725 but FASTA suggests not), len:564aa, similar eg. to S. pombe, FRP1_SCHPO, Q04800, ferric reductase transmembrane compon."	(AE000948) 3-hydroxyacyl-CoA dehydrogenase (hbd-10) [Archaeoglobus fulgidus]	(AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe]	Quinic acid utilization activator; regulatory protein QUTA - Emericella nidulans; (X06252) QUTA protein (AA 1 - 825) [Emericella nidulans]	(AL023533) hypothetical protein [Schizosaccharomyces pombe]
% cvrg 48	50	17	25		33	28		11
Blast Prob % id 2.00E-16 33 0.000000	02 2.00E-16 30	0.00002 32	0.000000 21 6	0.000000	1.00E-19 31	8.00E-48 38	0.000001	2.00E-11 51
Blast Score 85 59	69	49	54	63	26	190	53	47
aat Score 155 34	134	4	161	89	178	579	63	167
ncbi gi g115875 g1595750	g3914287	g2462747	g1723807	g2894292	g2648250	g3650382	g131767	g3130058
Database Hit ncbi gi g11587								
Selection Basis LINAP LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 461-479 430-450	682-705	493-512	438-457	805-829	710-735	722-744	459-478	270-289
. 2	22-48	23-46	29-48	28-48	109-128	22-48	43-61	115-132
Seq Primer and Contig source 5 pos 23841 ENU07635 ANI61C5903: 121-14 4961 4961 23842 ENU07636 ANI61C1747: 31-50	23221833 23843 ENU07637 ANI61C2775: 22-48	23844 ENU07638 ANI61C9628: 23-46 22502782	23845 ENU07639 ANI61C5931: 29-48 277690	23846 ENU07640 ANI61C1135 27:4071430	23847 ENU07641 ANIGIC1747: 109-128 710-735 35062751	23848 ENU07642 ANI61C9161: 22-48 12661	23849 ENU07643 ANI61C9628: 43-61 36964135	23850 ENU07644 ANI61C2801: 115-132 270-289 1321

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Description (U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans]; (U39847) AO66 ankyrin [Caenorhabditis elegans]	vegetatible incompatibility protein HET-E-1; (L28125) beta transducinlike protein [Podospora anserina]	vacuolar protein sorting-associated protein VPS5; (U73512) Vps5p [Saccharomyces cerevisiae]; (U84735) Vps5p [Saccharomyces cerevisiae]	hypothetical 85.0 KD protein in HLJ1-SMP2 intergenic region; hypothetical protein YMR164c - yeast (Saccharomyces cerevisiae); (Z49705) unknown [Saccharomyces cerevisiae]	TRNA splicing protein SPL1; (AF000115) tRNA splicing protein [Candida maltosa]	(Z99104) similar to cell-cycle protein [Bacillus subtilis]	(X71807) uric acid-xanthine permease [Emericella nidulans]	(AJ012627) haloalkane dehalogenase [Mycobacterium sp.]	(AL021839) putative nuclear pore protein [Schizosaccharomyces pombe]	(AC000133) ORF [Emericella nidulans]	(AL035065) putative urea active transporter [Schizosaccharomyces pombe]	hypothetical 59.1 KD protein ZK637.1 in chromosome III	"(X80835) len: 676, CAI: 0.13 [Saccharomyces cerevisiae]	(AL049498) rho1 gdp-gtp exchange protein 1 [Schizosaccharomyces pombe]
% cvrg 15		38		39		39	37	69	20	30		30	20
% id 34		34		1 72	_	92	28	30	1 28	48		25	4
Blast Prob 8.00E-41	3.00E-13	4.00E-18 34	0.0008	6.00E-78 72	0.000000	e-121	0.000000 28	3.00E-24 30	5.00E-24 28	2.00E-28 48	1.00E-11	4.00E-10 25	2.00E-94 64
Blast Score 167	75	97	4	290	61	392	41	112	111	109	70	65	346
aat Score 430	87	220	76	869	75	1908	94	326	245	339	57	141	1069
ncbi gi g1208874	g3023956	g2499128	g2497170	g2492879 698	g2632334	g3286685	g3860531	g2894271	g1870209	g4106690	£586797	g530340	g4539279 1069
Database Hit													
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 803-822	375-397	729-749	356-380	359-381	803-829		449-468	721-740	805-824	537-556	448-467	584-603	
Primer 5 pos 22-44	22-48	75-94	86-62	75-94	32-59		22-49	23-42	49-68	22-41	24-47	25-52	
Seq num Seq id Contig source 5 23851 ENU07645 ANI61C6552: 2 59294882	23852 ENU07646 ANI61C1137 2 9:40594439	23853 ENU07647 ANI61C1765: 75-94 8641	23854 ENU07648 ANI61C2801: 79-98 9591393	23855 ENU07649 ANI61C6608: 75-94 254836	23856 ENU07650 ANI61C1139 5:2041067	23857 ENU07651 ANI61C1807: 4801820	140: 1	23859 ENU07653 ANI61C1806: 3	ANI61C9147: 34714684	23861 ENU07655 ANI61C59:11 ; 36361	23862 ENU07656 ANI61C1140 3:689292	23863 ENU07657 ANI61C7181: 25-52 10941718	23864 ENU07658 ANI61C7196: 13841

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	(Saccharomyces cerevisiae); (Z48622) unknown [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps	purpureal choline-phosphate cytidylyltransferase (EC 2.7.7.15) - yeast (Saccharomyces cerevisiae); (Z49133) cholinephosphate cytidylyltransferase [Saccharomyces cerevisiae]; (Z72987) ORF YGR202c [Saccharomyces	cerevisiaej putative aconitase in PRP21-UBP12 intergenic region; aconitate hydratase homolog YIL200c - yeast (Saccharomyces cerevisiae); (X77688) hypothetical protein J0327 [Saccharomyces cerevisiae]; (Z49475) ORF YIL200c [Saccharomyces	cerevisiae] (AL034490) putative lectin precursor [Schizosaccharomyces nombe]	Actin; (AJ000335) actin [Botryotinia fuckeliana]	(AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] (U85909) peptide synthetase	[Aureobasidium pullulans] "Sp1/egr-like zinc-finger protein - fruit fly (Drosophila sp.); (S71230) Sp1/egr-like zinc-finger protein=hkb	[Drosophila, 0-4 hr embryos, Peptide, 296 aa] [Drosophila sp.]; huckebein gene [Drosophila melanogaster] " (AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]
% id cvrg		57	21	69	70	7 2	39	74
		55	4	40	86	32 42	32	47
Blast Prob 1.00E-18	0.000001	2.00E-69 55	1.00E-28 41	2.00E-32 40	e-145	1.00E-27 32 3.00E-40 42	4.00E-12 32	6.00E-29 47
Blast Score 79	52	178	126	111	513	123	71	94
aat Score 1356	124	640	204	296	1746	525	124	312
ncbi gi g2500542	g4499843	g2144437	g728783	g4008556	g3182891	g3510629 g4099313	g630885	g2459421
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 713-732	314-333	808-829	266-289	785-803	729-749	798-817	429-448	609-628
Primer 5 pos 32-58	92-99	22-49	28-50	45-64	22-42	23-50	22-44	23-50
Seq Prime num Seq id Contig source 5 pos 23865 ENU07659 ANI61C2840: 32-58 22811	23866 ENU07660 AM61C9655: 56-76	18271442 23867 ENU07661 ANI61C6602: 22-49 8291979	23868 ENU07662 ANI61C2875: 28-50 978595	23869 ENU07663 ANI61C9645: 45-64	23870 ENU07664 ANI61C183:1 22-42 1371	23871 ENU07665 ANI61C2835: 23-50 12645 23872 ENI107666 ANI61C9163: 23-49	6161967 23873 ENU07667 ANIGIC6535: 22-44 99969601	23874 ENU07668 ANI61C1758: 23-50

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Description "mitochondrial nuclease; nuclease NUC1 (EC 3.1.30-) precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (X06670) nuclease [Saccharomyces cerevisiae]; (Z34098) ORF [Saccharomyces cerevisiae]; (X77688) mitochondrial nuclease [Saccharomyces cerevisiae]; (Z49483) ORF YIL208c [Saccharomyces	DNA-directed RNA polymerase mitochondrial precursor; (L.25087) mitochondrial RNA polymerase [Neurospora crassa]; cyt-5 gene	Chromodomain-helicase-DNA-binding protein 1 (CHD-1); (L10410) DNA-hinding protein [Mass musculus]	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region; (AE000443) orf, hypothetical protein [Escherichia coli] "	hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region; probable resistance protein - yeast (Saccharomyces cerevisiae); (Z36049) ORF YBR180w [Saccharomyces	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c	(299260) probable na(+)-h(+) antiporter [Schizosaccharomyces pombe]
% id cvrg			26	37		37
	<b>,</b> 0		2 27	4 24	C	92 0
Blast Prob 5.00E-67	6.00E-26	0.33	9.00E-22	6.00E-14 24	4.00E-10	2.00E-90 58
Blast Score 200	118	35	103	55	92	332
aat Score 641	139	116	181	107	<i>L</i> 9	886
ncbi gi g128831	g730615	g1345773 116	g2851420 181	g586312	g2132942	g2414637
n Database Hit						
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 363-380	795-815	491-510	561-580	622-641	422-441	744-767
Primer 5 pos 222-241	22-45	110-137	22-45	36-53	22-49	26-53
Contig source 2 ANI61C9146: 2 1595	ANI61C9678: 3	ANI61C6535: 90398508	2 ANI61C59:45	33062556	485850	36912752
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 23875 ENU07669 ANI61C9146: 222-241 363-380 1595	23876 ENU07670 ANI61C9678: 22-45 10011846	23877 ENU07671 ANI61C6535: 110-137 491-510 90398508	23878 ENU07672 ANI61C59:45 22-45 755192	23879 ENU07673 ANI61C7187: 36-53 33062556	23880 ENU07674 ANI61C6605: 22-49 485850	23881 ENU07675 ANI61C5928: 26-53 36912752

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Description GAA1 protein; membrane protein END2 - yeast (Saccharomyces cerevisiae); (X79409) Gaa1 [Saccharomyces cerevisiae]; (U53880) Gaa1p [Saccharomyces cerevisiae]; (Z73260) ORF YLR088w [Saccharomyces cerevisiae]	(AJ22399) PCZA363.5 [Amycolatopsis orientalis] (M77661) putative pol polyprotein [Magnanorthe grisea]	hypothetical 50.6 KD protein in RPL14B-GPA1 intergenic region; hypothetical protein YHR004c - yeast (Saccharomyces cerevisiae); (U10555) Yhr004cp (Saccharomyces cerevisiae)	(AL049521) hypothetical protein [Schizosaccharomyces pombe]	(AB015510) FII-CMCase [Aspergillus aculeatus]	hypothetical 65.3 KD protein in PRE3-SAG1 intergenic region; hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae); (X87611) ORF YJR83.4 [Saccharomyces cerevisiae]; (Z49501) ORF YJR001w [Saccharomyces cerevisiae]	(AL023592) ma binding protein [Schizosaccharomyces pombe]	"N2,N2-dimethylguanosine TRNA methyltransferase precursor; N2,N2-dimethylguanine tRNA methyltransferase - yeast (Saccharomyces cerevisiae); (M17193) tRNA dimethyltransferase [Saccharomyces cerevisiae]; (Z48758) Trmlp [Saccharomyces cerevisiae] "
% id cvrg 38 42	6 20	53	46	27	27	19	42
Blast Prob 3.00E-41	0.000000 30 04 2.00E-43 39	5.00E-34 41	1.00E-41 35	2.00E-23 57	4.00E-31 39	1.00E-19 27	1.00E-34 42
Blast Score 142	58 176	94	115	87	134	86	146
aat Score 403	71 463	339	458	262	302	194	781
ncbi gi g729417	g2894190 g538067	g731630	g4539592	g3242653	g1353046 302	g3136059	g136242
Database Hit ncbi gi g72941							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 808-829	451-470	781-808	771-790	453-479	454-478	723-749	611-630 LINAP
Primer 5 pos 23-42	22-49	28-47	35-54	117-137	107-127	22-41	29-50
Seq num Seq id Contig source 5 23882 ENU07676 ANI61C1139 2 7:41762829	23883 ENU07677 ANI61C6605: 22-49 17772165 23884 ENU07678 ANI61C1136: 63-90	23885 ENU07679 ANIGLC2838: 28-47 44065240	23886 ENU07680 ANI61C9153: 35-54 34112201	23887 ENU07681 ANI61C6623: 117-137 453-479 4301	23888 ENU07682 ANI61C5970: 107-127 454-478 3781	23889 ENU07683 ANI61C1139 39:33064594	23890 ENU07684 ANI61C7223: 29-50 16061

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Description hypothetical 79.4 KD protein in PRP16-SRP40 intergenic region; (Z28315) ORF YKR090w	(Z79695) Similarity to Human 2-oxoisovalerate dehydrogenase (SW:ODBB_HUMAN)	alpha-L-arabinofuranosidase precursor (arabinosidase); (AL021411) arabinofuranosidase [Streptomyces	(Z93938) unknown [Bacillus subtilis]	(AL034382) hypothetical protein [Schizosaccharomyces pombe]	(AL031603) 60s ribosomal protein [Schizosaccharomyces pombe]	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae);	[Saccharomyces cerevisiae] hypothetical 36.5 KD protein in GBSA-TLPB intergenic region; (Z99119) similar to hypothetical	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5- FET4 intergenic region; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae); (Z54141)	(AF091042) putative cercosporin	(Y11113) endoglucanase IV [Hypocrea jecorina]
% cvrg 22	89	24	47		43	36	4	59	24	46
Blast Prob % id 4.00E-24 36	5.00E-47 53	0.000003 47	0.000008 30	0.23	3.00E-17 73	1.00E-26 32	1.00E-12 33	5.00E-35 47	8.00E-11 41	4.00E-17 40
Blast Score 111	138	44	20	36	88	120	73	113	<i>L</i> 9	88
aat Score 94	843	128	71	52	436	271	122	413	196	159
ncbi gi g1176495	g3876393	g3912958	g1934826	g3947870	g3646455	g1730644	g3915558	g2492777 413	g3885836	g2315274
Database Hit										
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 445-465	772-799	452-471	452-479	457-479	448-475	665-684	430-449	519-546	453-480	456-475
Primer 5 pos 22-45	22-42	22-47	34-53	30-57	39-58	56-75	68-87	26-45	44-64	52-71
Contig source ANI61C6601: 39303485	23892 ENU07686 ANI61C9170: 22-42 36674819	23893 ENU07687 ANI61C9674: 22-47 807441	23894 ENU07688 ANI61C1139: 34-53	ANI61C9184:	33:	23897 ENU07691 ANI61C5982: 56-75 1258541	23898 ENU07692 ANI61C1139: 68-87 27582293	23899 ENU07693 ANI61C1869: 26-45 6621	23900 ENU07694 ANI61C5985: 44-64	23901 ENU07695 ANI61C1907: 52-71 5341
Seq id 1 ENU07685	2 ENU07686	3 ENU07687	4 ENU07688	5 ENU07689	6 ENU07690	7 ENU07691	8 ENU07692	9 ENU07693	0 ENU07694	1 ENU07695
Seq num 23891	23892	23892	23894	23895	2389(	2389	2389{	23899	2390	2390

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% id cvrg Description	(AL034353) glutamate n- acetyltransferase precursor	adducin 1 (alpha); (Z68280) Human tetracycline transporter-like protein mRNA [Homo sapiens]	carbonyl reductase 3; (AB004854) carbonyl reductase 3 [Homo sapiens]; (AB003151) carbonyl reductase 3 [Homo saniens]	probable transcription factor YPL230w probable transcription factor (X94561) transcription factor [Saccharomyces cerevisiae]; (Z73586) ORF YPL230w [Saccharomyces	(U07801) serine/threonine/tyrosine kinase [Ustilago maydis]	(AL021767) hypothetical protein [Schizosaccharomyces pombe]	(AE000755) transketolase [Aquifex aeolicus]	"mitochondrial 60S ribosomal protein L24 precursor (YML24); ribosomal protein YmL24, mitochondrial - yeast (Saccharomyces cerevisiae); (Z47815) ribosomal protein [Saccharomyces cerevisiae] "	(L27993) alkaline phosphatase [Neurospora crassa]	(Z81360) hypothetical protein Rv1726 [Mycobacterium tuberculosis]	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region; (AE000443) orf, hypothetical protein [Escherichia coli] "
% cvrg	32	41	53	4	33	92	18	2	47	20	33
% id 24	49	40	32	33	4	48	35	40	61	27	56
Blast Prob	6.00E-30 49	6.00E-13 40	3.00E-15 32	6.00E-17 33	1.00E-21 44	2.00E-11 48	0.000000 35	1.00E-28 40	3.00E-88 61	0.000000 27 009	6.00E-79 56
Blast	130	75	83	83	71	69	09	126	286	61	178
aat Score 55	263	252	168	178	220	130	51	254	939	178	1248
	g3925783	g4501925	g4502601 168	g2133058	g476334	g2853097	g2984067	g1350795	g450864	g1654028	g2851420 1248
Database Hit ncbi gi											
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 452-479	457-479	578-603	458-477		454-479		454-481	420-439	722-741	644-663	731-750
Primer 5 pos 23-50	32-51	22-46	26-45		: 106-124		: 25-52	: 54-74	: 22-46	: 26-48	: 38-57
Seq num Seq id Contig source 23902 ENU07696 ANI61C9180:	23903 ENU07697 ANI61C5987: 5761052	23904 ENU07698 ANI61C1143 0:27333362	23905 ENU07699 ANI61C1142 7:9971438	23906 ENU07700 ANI61C9663: 54325009	23907 ENU07701 ANI61C2977: 106-124 454-479	23908 ENU07702 ANI61C7261: 13631008	23909 ENU07703 ANI61C6642: 25-52 106607	23910 ENU07704 ANI61C2968: 54-74 1245741	23911 ENU07705 ANI61C6595: 22-46 10211	23912 ENU07706 ANI61C5991: 26-48 1321625	23913 ENU07707 ANI61C1894: 38-57 24394124

Description (Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis] beta3A-adaptin; (U91931) AP-3 complex beta3A subunit [Homo	(AL031262) hypothetical protein [Schizosaccharomyces pombe] Ethanolamine kinase (easily shocked protein); (L35603) ethanolamine kinase [Drosophila melanogaster]	(AL033389) putative aminotransferase (AL033389) putative aminotransferase [Schizosaccharomyces pombe] hypothetical 108.0 KD helicase in HSP26-TIF32 intergenic region; probable DNA repair protein - yeast (Saccharomyces cerevisiae); (X76294) ORF YBRO715; homologous to Rad54 Snf2 and Sth1 of S.cerevisiae [Saccharomyces cerevisiae]; (Z35942) ORF YBR073w [Saccharomyces	cerevisiae] putative transcription initiation factor TFIID 111 KD subunit (TBP-associated factor 111 KD) (TAFII-111); hypothetical protein SPAC2G11.14 - fission yeast (Schizosaccharomyces pombe); (Z54354) putative transcription initiation factor tfiid	subunit [Schizosaccharomyces pombe] "(U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramecium bursaria	Chlorella virus 1] chitin deacetylase - Mucor rouxii (fragment) (AL035548) hypothetical protein [Schizosaccharomyces pombe]
% cvrg	32	28 28	28		36
Blast Prob % id 4.00E-17 31 0.002	0.0005 0.000000 31 003	2.00E-37 43 1.00E-35 45	5.00E-49 43	0.0004	1.00E-14 29 9.00E-29 34
Blast Score 68 43	45	118	170	45	80
aat Score 134 80	94	319	1182	80	123 371
ncbi gi g1806234 g4501975	g3417427 g1706559	g3850091	g1174555	g624076	g1085697 g4456816
Database Hit					
Selection Basis LINAP LINAP	LINAP LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 481-502 705-732	453-479	585-604	719-737	531-551	454-478
Primer 5 pos 24-43 22-45	22-49	27-47	23-48	38-57	24-43
Seq num Seq id Contig source : 23914 ENU07708 ANI61C9673: 58285111 23915 ENU07709 ANI61C5961: 28042047	23916 ENU07710 ANI61C1036 22-49 3:12461693 23917 ENU07711 ANI61C2978: 63-90 6681	23918 ENU07712 ANI61C9701: 27-47 32063928 23919 ENU07713 ANI61C6593: 23021	23920 ENU07714 ANI61C599:2 23-48 2471	23921 ENU07715 ANI61C1044 3:20022587	23922 ENU07716 ANI61C9675: 24-43 57446242 23923 ENU07717 ANI61C5953: 24-43 993555

Description (Z34801) Similarity with drosohila MSP-300 protein (PR acc. no. S30431) [Caenorhabditis elegans]; (Z66514) Similarity with drosohila MSP-300 protein (PR acc. no. S30431) [Caenorhabditis elegans]	(X93302) Msn5 protein [Saccharomyces cerevisiae]	(AF111068) DNA polymerase gamma [Neurospora crassa]	"alcohol dehydrogenase (ADH-T); alcohol dehydrogenase (EC 1.1.1.1), thermostable - Bacillus stearothermophilus; (D90421) alcohol dehydrogenase [Bacillus stearothermophilus] "	(AB001895) B120 [Homo sapiens]	(AL023534) hypothetical protein [Schizosaccharomyces pombe]	(AF051140) putative glucose transporter protein [Schizosaccharomyces pombe]	"(AE001002) ATP-dependent RNA helicase, putative [Archaeoglobus fulgidus]"	hypothetical 93.9 KD helicase C19G10.02 in chromosome I; (Z69909) dna repair protein [Schizosaccharomyces pombe]	(AL022600) hypothetical protein [Schizosaccharomyces pombe]	hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region; probable membrane protein YML059c - yeast (Saccharomyces cerevisiae); (Z46729) unknown [Saccharomyces cerevisiae]
% cvrg 24	;	71	65		29	36	35	27	33	16
% id 21		/0	34		40	27	33	47	. 42	45
Blast Prob 0.008	0.000000	e-104	9.00E-17 34	0.12	2.00E-32 40	0.000000 27 04	3.00E-31 33	6.00E-47 47	5.00E-34 42	9.00E-53 42
Blast Score 41	61	3//	53	38	129	59	119	187	145	207
aat Score 130	411		270	148	348	135	798	371	258	596
ncbi gi g3877858	g1246837	g445500/	g1168347	g2588991	g3130035	g3746450	g2649107	g1723497	g3080533	g2501686
Database Hit										
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 778-798	805-829	802-829		804-823	471-490	773-796	791-810	99-999	761-780	723-742
Primer 5 pos 22-48	59-56	22-49		24-43	102-120	22-44	40-59	87-106	39-62	26-53
Prime Seq id Contig source 5 pos ENU07718 ANI61C2959: 22-48 11071	23925 ENU07719 ANI61C9693: 29-56 3518378	23926 ENU07720 ANI61C7224: 22-49 3886663	23927 ENU07721 ANI61C6624: 41971	23928 ENU07722 ANI61C1059 3	23929 ENU07723 ANI61C3017: 102-120 471-490 1011410	23930 ENU07724 ANI61C9716: 22-44 9471	23931 ENU07725 ANI61C6617: 40-59 18203569	23932 ENU07726 ANI61C6009: 87-106 1244451	23933 ENU07727 ANI61C6621: 39-62 46203659	23934 ENU07728 ANI61C600:1 26-53 2731
Seq num Seq 23924 EN	23925 EN	23926 EN	23927 EN	23928 EN	23929 EN	23930 EN	23931 EN	23932 EN	23933 EN	23934 EN

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	o [Kaistollia europhia] (U77581) sugar transporter 3 [Pichia	supuss "Dynein heavy chain, cytosolic (DYHC); cytoplasmic dynein heavy chain - Emericella nidulans; (U03904) cytoplasmic dynein [Emericella	nidulans]" (AL021748) hypothetical protein	locinzosaccharomyces pomoej hypothetical 180.2 KD protein in FAA4-HOR7 intergenic region; probable membrane protein YMR247c	- yeast (Saccharomyces cerevisiae) "112.3 KD protein in PYK1-SNC1 intergenic region; FUN12 protein - yeast (Saccharomyces cerevisiae); (U12980) Fun12p: 97kDa protein, function unknown [Saccharomyces	cerevisiae] " (U81794) putative permease [Hromwees fahae]	40S ribosomal protein S7; (U73847) ribosomal protein fNeurospora crassal	ATP-dependent proteinase BsgA -	GRR1 protein; GRR1 protein - yeast (Saccharomyces cerevisiae); (MS9247) putative [Saccharomyces cerevisiae]; (Z49590) ORF YJR090c [Saccharomyces cerevisiae]; (L47993)	OKF 1 JROYOC [Sacchalonnyces cerevisiae] (D63905) ubiquitin ligase [Saccharomyces cerevisiae]
% cvrg 22	19	9	15	15			73	27	17	11
% id 9.36	35	96	45	, 26			11 (	54	7 31	31
Blast Prob % i 5.00E-10 36	7.00E-12	e-135	1.00E-22 45	3.00E-13 26	0.00005	0.004	1.00E-50 77	3.00E-51 54	8.00E-17 31	3.00E-12 31
Blast Score 64	71	321	106	48	39	41	155	136	51	71
aat Score 94	132	5402	204	164	107	51	714	575	150	141
ncbi gi g2120949	g4098421	g1169440	g2842510	g2497203 164	g1723187	g1764098	g3929366	g625653	g121649	g2257705 141
Database Hit ncbi gi g21209										
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 413-432	427-454	737-764	409-433	735-759		442-467	403-425	655-673	439-466	366-385
Primer 5 pos 34-53	22-47	22-49	37-58	68-87		122-145	32-52	33-52	22-48	22-45
Seq num Seq id Contig source 23935 ENU07729 ANI61C6011: 6101027	23936 ENU07730 ANI61C6030: 22-47	340040 23937 ENU07731 ANI61C3004: 22-49 3923781	23938 ENU07732 ANI61C972:1 37-58	53368 23939 ENU07733 ANI61C9702: 68-87 32944074	23940 ENU07734 ANI61C6675: 9181244	23941 ENU07735 ANI61C1136 122-145 442-467	23942 ENU07736 ANI61C9235: 32-52	86:	23944 ENU07738 ANI61C9700: 22-48 49655613	23945 ENU07739 ANI61C1500: 22-45 1428

Decription		(Z99532) hypothetical protein [Schizosaccharomyces pombe]	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "	SSO2 protein; syntaxin-related protein SSO2 - yeast (Saccharomyces cerevisiae); (Z49808) unknown Saccharomyces cerevisiae)	(AF001630) SH3P18-like WASP associated protein [Homo sapiens]	CAMP binding protein CABP1A/CABP1B (CABP1 protein); CABP1 protein - slime mold	(Dictyostelium discoideum); (X52688) CABP1 protein [Dictyostelium discoideum]; (M36176) cAMP binding	protein [Dictyostelium discoideum] (AL033497) unknown hypothetical	protein [Candida albicans] ryanodine receptor [Oryctolagus cuniculus]	(Z99714) bK1048E9.2 (similar to CE02118) [Homo sapiens]	6-hydroxy-D-nicotine oxidase (6- HDNO); (X05999) 6-hydroxy-D- nicotine oxidase [Arthrobacter oxidans]	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium]	(Ú53876) Cdc45p: assembles into a complex with Cdc46p/Mcm5p [Saccharomyces cerevisiae]	transcription factor nft1 - fission yeast (Schizosaccharomyces pombe)
%	27 27	17	14	76	27			12	2	31	23	10		16
Pi %	30	34	26	23	32			34	28	1 22	39	0 21		0 26
Blast		8.00E-21	0.0008	0.00007	0.000000 32	0.004		0.00002	0.0004	6.00E-14 22	0.000000 39	0.000000 21	0.85	0.000000 26 7
Blast		100	4	48	62	41		48	45	78	62	4	34	24
aat Score	3001E	195	80	08	6	46		104	88	137	170	98	202	69
ido ig	g2887409	g4582195	g1166378	g1711542	g4100623	g115573		g3859703	g226386	g4455408	g122805	g2147662	g1256852	g626072
l Dotobose Hit	Database mit													
Selection	Dasis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer	5 pos 639-658	381-399	262-289	745-765	414-433	457-476		293-312	594-613	413-434	277-299	809-829	520-539	457-477
Primer 5 200	3 pos 22-49	116-135	47-73	22-40	62-81	22-43		102-126	40-59	44-68	39-58	69-05	70-92	22-42
bi oco	num Seq 1d Coling Source 23946 ENU07740 ANI61C7292: 1197496	23947 ENU07741 ANI61C6688: 116-135 381-399 9071343	23948 ENU07742 ANI61C1432: 47-73 34163809	23949 ENU07743 ANI61C9221: 22-40 5921377	23950 ENU07744 ANI61C9697: 62-81 47004381	23951 ENU07745 ANIGIC7292: 16441233		23952 ENU07746 ANI61C6692: 102-126 293-312	1345 23953 ENU07747 ANI61C1726: 40-59 9031554	23954 ENU07748 ANIGLC6692: 44-68 9541488	23955 ENU07749 ANI61C3030: 39-58 16891370	23956 ENU07750 ANI61C923:3 50-69 4572487	23957 ENU07751 ANI61C9750: 70-92 1120549	23958 ENU07752 ANI61C7276: 22-42 717341

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Description 60S ribosomal protein L27; ribosomal protein L27 - fungus (Filobasidium floriforme); (L37877) ribosomal protein L27 [Filobasidiella	(Z99296) hypothetical protein [Schizosaccharomyces pombe] (AB004537) hypothetical protein YPL063w [Schizosaccharomyces	pombe] "transcription factor HCM1 - yeast (Saccharomyces cerevisiae); (X59720) YCR065w, len:532 [Saccharomyces	Cerevisiae) (D86478) Crb2 [Schizosaccharomyces nombe]	(AF025410) cephalosporin esterase	precursor (knodospordium torutoides) (AL021086) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=150.57; 1-evidence_end; 2-evidence=predicted by match; 2-match accession=AI238311;	2-match_description=GH14334.5prime GH Drosophila melanogaste hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession car	phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
% cvrg 61	10		41	38	17		43
% id	31		32	35	) 33		1 34
Blast Prob % 5.00E-17 43	5.00E-31 31 8.00E-55 50	5.00E-10	0.000000 32	7.00E-23 35	0.000000 33 003	1.00E-15	9.00E-31 34
Blast Score 88	131	49	58	107	62	84	126
aat Score 163	909	96	79	196	72	118	339
ncbi gi g1173005	g2414649 909 g2257530 502	g83245	g1449177	g2731568	g2749755	g2132293	g3702646 339
Database Hit							
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 451-470	797-816	459-479	281-307	629-656	553-580	699-718	
Primer 5 pos 29-52	32-51	23-50	122-144	102-121	102-121	43-62	
Seq id Contig source 59 ENU07753 ANI61C9246: 10721418	23960 ENU07754 ANI61C9740: 32-51 12223 23961 ENU07755 ANI61C6597: 22-41 7481	23962 ENU07756 ANI61C1963: 23-50 3981	23963 ENU07757 ANI61C9246: 122-144 281-307	23964 ENU07758 ANIGIC9698: 102-121 629-656	1685 23965 ENU07759 ANI61C9209: 102-121 553-580 1611	23966 ENU07760 ANI61C3796: 43-62 4911252	23967 ENU07761 ANI61C3052: 6221558
Seq num 2395	2396	2390	2396	2396	2390	2396	239(

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Description hypothetical 77.3 KD protein in FIG1- GIP1 intergenic region; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae); (Z35912) ORF YBR043c [Saccharomyces	(AB004537) lipoate-protein ligase A [Schizosaccharomyces pombe] (AL035226) guanine nucleotide binding protein beta subunit-like	[Schizosaccharomyces pombe] (AL022299) hypothetical protein [Schizosaccharomyces pombe] Integrin alpha chain-like protein (alpha-INT1); (U35070) integrin-like protein	alpha Intlp [Candida albicans] putative AC transposase (ORFA); (X05424) ORFa [Zea mays] "putative 108.8 KD transcriptional regulatory protein in FKH1-STH1 intergenic region; probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae); (Z38059) orf, len: 964, CAI: 0.15, possible	regulatory protein [Saccharonnyces cerevisiae] " "probable ATP-dependent permease precursor; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae); (X59720) YCR011c, len:1049 [Saccharomyces	cerevisiae] " (U71107) S-adenosyl-methionine- sterol-C-methyltransferase homolog	[X28980] hypothetical protein [Schizosaccharomyces pombe]
% cvrg 24	57	37	30	25	34	74
% id 23	43 34	54	30	55	31	69
Blast Prob % 4.00E-10 23	2.00E-38 4.00E-11	2.00E-37 54 0.000000 34 05	9.00E-19 30 2.00E-10	4.00E-41 55	0.00002	4.00E-72 69
Blast Score 65	159	100	94	168	50	271
aat Score 114	319	352	991	1374 168	106	734
ncbi gi g586486	g2257523 g4160573	g3006139 g1708501	g136125 g731872	g113449	g2246452	g2656003
Database Hit ncbi gi g58648						
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 528-546	627-649	440-459	768-790	796-815	629-099	758-779
Primer 5 pos 22-49	22-49	22-41	67-94 111-130	22-40	22-44	33-53
Contig source 7762 ANI61C3806: 15762142	23969 ENU07763 ANI61C6661: 22-49 10801751 23970 ENU07764 ANI61C297:9 74410255	23971 ENU07765 ANI61C3818: 22-41 23911914 23972 ENU07766 ANI61C9698: 22-43 80978486	23973 ENU07767 ANIGIC7307: 67-94 768-790 5231333 23974 ENU07768 ANIGIC6716: 111-130 341-360 25202076	23975 ENU07769 ANI61C1918: 22-40 2568660	23976 ENU07770 ANI61C3066: 22-44 879134	23977 ENU07771 ANI61C9727: 33-53 6421451
q m Seq id 968 ENUO	969 ENUC 970 ENUC	971 ENUC 972 ENUC	973 ENU( 974 ENU(	975 ENU(	976 ENU(	977 ENU(
Seq num 2396	23.	23.	23 23	23	23	23

	(AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens] "(U80668) homogentisate 1,2-	dioxygenase [Arabidopsis thaliana] " (D87686) KIAA0017 protein [Homo sapiens]	hypothetical protein KIAA0210; (D86965) similar to a putative protein coded in Caenorhabditis elegans cosmid B0393. [Homo sapiens]	hypothetical protein YLR357w - yeast (Saccharomyces cerevisiae); (U19102) Ylr357wp [Saccharomyces cerevisiae]	probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin); (AL023859) putative ubiquitin protein ligase [Schizosaccharomyces pombe]	alpha-glucosidase precursor (maltase); (D86624) alpha-glucosidase precoursor [Spinacia oleracea]	G1/S-specific cyclin PCL1 (cyclin HCS26); cyclin G1 homolog HCS26 - yeast (Saccharomyces cerevisiae); (M73966) G1 cyclin [Saccharomyces cerevisiae]; (Z71565) ORF YNL289w [Saccharomyces cerevisiae]	N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease - Neurospora crassa; (L34605) neutral amino acid permease [Neurospora
	22	19	20	31	4	23	63	50
Blast Prob % id 5.00E-16 36	1.00E-22 36 2.00E-16 43	8.00E-56 51	6.00E-20 35	2.00E-62 40	9.00E-49 40	6.00E-48 48	2.00E-32 47	7.00E-10 31
<b>v</b>	106 J 85 2	217 8	69	239 2	5 0/1	115	139	. 59
ي	405 159	705	173		905	426	297	182
ncbi gi g731298	g2801701 g4098647	g3540219	g2495720	g1077415 529	g3915187 902	g3023260 426	g116149	g2507070 182
Database Hit								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 563-584	592-611		549-576		811-829	724-749	363-383	784-803
Primer 5 pos 22-49	23-50		61-84		43-62	22-46	25-48	22-42
Seq Prime num Seq id Contig source 5 pos 23978 ENU07772 ANI61C6686: 22-49 981219	23979 ENU07773 ANI61C3047: 23-50 592-611 1105347 23980 ENU07774 ANI61C3850: 117-136 282-303	1334 23981 ENU07775 ANI61C311:1 380679	23982 ENU07776 ANI61C7345: 61-84 1597	23983 ENU07777 ANI61C6723: 1583570	23984 ENU07778 ANI61C1952: 43-62 12692376	23985 ENU07779 ANI61C9727: 22-46 46815583	23986 ENU07780 ANI61C7285: 25-48 32653862	23987 ENU07781 ANI61C298:5 22-42 8914773

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Seq         Primer         Primer         Selection         ant         Blast         Blast         %           23988         ENUO7783         ANIGIC3844:         57.76         620-643         LINAP         Basis         Database Hit nebi gi         Score         Score         Prob         % id cvrg           23988         ENUO7783         ANIGIC3944:         57.76         620-643         LINAP         g3874557         356         166         1.00E-40         45         25           23990         ENUO7784         ANIGIC2092:         2.2.45         443-469         LINAP         g671684         1353         200         1.00E-50         40         32           23991         ENUO7784         ANIGIC209:         2.2.45         440-467         LINAP         g2660584         111         39         0.021         37           23992         ENUO7786         ANIGIC209:         2.2-46         LINAP         g4490979         117         52         0.000004         35         53           23992         ENUO7787         ANIGIC2078:         2.2-463         LINAP         g4490979         136         83         2.00E-14         118           23994         ENUO7789         ANIGIC2010:         2.	synthase [Colletotrichum lagenarium]
Primer         Selection         Basis         Database Hit g1363740         Score Score Prob Score Prob Score Score Score Prob Score Score Score Prob Score Score Score Score Prob Score	
Primer         Selection         aat         Blast           3 pos         Basis         Database Hit         ncbi gi         Score         Score           620-643         LINAP         g1363740         157         76           513-540         LINAP         g3874557         356         166           443-469         LINAP         g2660584         111         39           440-467         LINAP         g118239         117         52           637-656         LINAP         g4490979         136         83           709-730         LINAP         g2739028         115         57           436-455         LINAP         g114866         55         57           808-535         LINAP         g2408014         186         106           789-808         LINAP         g2147662         987         145	
Primer         Selection         aat         Blast           3 pos         Basis         Database Hit         ncbi gi         Score         Score           620-643         LINAP         g1363740         157         76           513-540         LINAP         g3874557         356         166           443-469         LINAP         g2660584         111         39           440-467         LINAP         g118239         117         52           637-656         LINAP         g4490979         136         83           709-730         LINAP         g2739028         115         57           436-455         LINAP         g114866         55         57           808-535         LINAP         g2408014         186         106           789-808         LINAP         g2147662         987         145	
Frimer Selection 3 pos Basis Database Hit ncbi gi Score 620-643 LINAP g1363740 157  513-540 LINAP g2660584 111  440-467 LINAP g118239 117  621-643 LINAP g2739028 115  709-730 LINAP g2739028 115  436-455 LINAP g2739028 115  436-455 LINAP g2739028 115  738-835 LINAP g2408014 186	
Frimer Selection 3 pos Basis Database Hit ncbi gi 620-643 LINAP g1363740 g13-540 LINAP g2660584 443-469 LINAP g2660584 440-467 LINAP g118239 g21-643 LINAP g2739028 g21-643 LINAP g2739028 g21-643 LINAP g2739028 g21-643 LINAP g2739028 g21-645 LINAP g2739028 g2408014 g28-808 LINAP g2147662	
Frimer Selection 3 pos Basis Database Hit 1620-643 LINAP 799-825 LINAP 443-469 LINAP 621-643 LINAP 709-730 LINAP	
Frimer Selection 3 pos Basis Database Hit 1620-643 LINAP 799-825 LINAP 443-469 LINAP 621-643 LINAP 709-730 LINAP	
799-825 LINAP 799-825 LINAP 443-469 LINAP 440-467 LINAP 621-643 LINAP 709-730 LINAP 709-730 LINAP 709-730 LINAP 709-730 LINAP 709-730 LINAP 709-730 LINAP	
3 pos 620-643 620-643 799-825 443-469 440-467 637-656 621-643 709-730 436-455 508-535 789-808	
Prin Contig source 5 pc 2 ANI61C3844: 57-7 3791042 3791042 3611 5611 5611 5611 5611 8 ANI61C298:7 23-4 839831 839831 839831 839831 83504811 80 ANI61C2731: 38-3 41534547 41534547 523 6001 223 2937774	
Contig source 3791042 3791042 3791042 3791042 3611 36175527 3611 37472 3611 3791042 3791042 3611 36175527 3611 3791042 3791042 3611 3791042 3791042 37472 37472 37472 37472 37472 37472 37472 37472 37472 37472 375774	
Contig s 37910 37910 37910 3611 5611 5611 57 ANIG1C 83983 11975 18 ANIG1C 14582 19 ANIG1C 14582 11975 11 ANIG1C 29377	
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Seq num Seq id 23988 ENU07782 23990 ENU07784 23991 ENU07785 23992 ENU07787 23994 ENU07789 23995 ENU07790 23997 ENU07791 23998 ENU07791 23998 ENU07792	
88 S6 D0 E7 B E8	
Seq num 2398 2399 2399 2399 2399 2399 2399 2399	

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	Description hypothetical protein 471 - Rhizobium leguminosarum; (X77198) orf471; homologous to NodT [Rhizobium leguminosarum]	"DLTE protein; hypothetical protein-Bacillus subtilis; dltE productlputative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa]; (X73124) ipa-1r [Bacillus subtilis]; (Z99123) alternate gene name: ipa-1r [Bacillus subtilis]"	(Z99296) hypothetical protein [Schizosaccharomyces pombe]	DNA repair protein RAD13; excision repair protein - fission yeast (Schizosaccharomyces pombe); (X66795) excision repair protein	(X94215) MSP8 [Saccharomyces cerevisiae]	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "	"(AF091251) Ybt peptide/polyketide synthetase HMWP1 [Yersinia pestis]; (AL031866) ORF68, Ien=3163 aa,	irp1, function=synthesis of siderophore yersiniabactin, product=HMWP1 protein, 97.9% identity in 3163 aa overlap to YEIRPOP_1 Y.enterocolitica irp1, Fasta scores: opt: 2088 EO: 0 [Yersinia pestis] "	(U28943) similar to hydratasedehydrogenase-epimerase (HDE)	TOXD protein; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
B	% id cvrg		10	24		4	3		69	89
	% id		29	47		36	4		40	38
Blact		4.00E-22	1.00E-25 29	3.00E-60 47	0.013	2.00E-23 36	2.00E-11 44		2.00E-13 40	3.00E-24 38
Blact		104	116	232	39	108	89		75	112
•	Score	138	471	898	39	4	166		170	244
	ncbi gi g541015	g729344	g2414649	g131777	g1122901	g1166378	g3818605		g861336	g1729996 244
,	Database Hit									
Cologica	Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP
Drimer	3 pos 804-829	535-554	707-730	771-790	330-349	407-426	311-330		804-826	571-590
Drimer	5 pos 24-43	22-44	22-45	22-41	112-131	51-70	121-140		32-51	22-44
	Contig source : ANI61C7926: 2051472	ANI61C7335: 2	ANI61C3863: 28061	ANI61C7355: 3	ANI61C380:1	ANI61C7962:	ANI61C6708: 1380		ANI61C31:1 949	ANI61C9759: 1593957
ć	23999 ENU07793 ANI61C7926: 24-43 2051472	24000 ENU07794 ANI61C7335: 22-44 20142622	24001 ENU07795 ANI61C3863: 22-45 28061	24002 ENU07796 ANI61C7355: 22-41 13012388	24003 ENU07797 ANI61C380:1 112-131 330-349	24004 ENU07798 ANIGIC7962: 51-70	24005 ENU07799 ANIGIC6708: 121-140 311-330 1380		24006 ENU07800 ANI61C31:1 32-51 949	24007 ENU07801 ANI61C9759: 22-44 1593957

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Description 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (HMG-COA reductase 2); hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) II - yeast (Saccharomyces cerevisiae); (M22255) 3-hydroxy-3-methyl glutaryl coenzyme A reductase [Saccharomyces cerevisiae]; (U22382) Hmg2p: 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase	(AF079317) unknown [Sphingomonas	geranylgeranyl transferase type I beta subunit (type I protein geranyl-geranyltransferase beta subunit) (GGTASE-I-beta); geranylgeranyl-diphosphate geranylgeranylgeranyltransferase (EC 2.5.1.32) I beta chain - rat; (L24116) geranylgeranyltransferase transferase transferase transferase transferase transferase	probable kynureninase (L-kynurenine hydrolase); (U56965) similar to R. norvegicus kynureninase (PIR:PS0370)	(AL031644) RAD16 nucleotide excision repair protein homolog	(AL031764) putative helicase [Schizosaccharomyces pombe]	fumarate reductase (NADH) (EC 1.3.1.6) - yeast (Saccharomyces cerevisiae)	(X97581) spalt protein [Mus musculus]	hypothetical 17.3 KD protein in ERP5-ORC6 intergenic region; hypothetical protein YHR116w - yeast (Saccharomyces cerevisiae); (U00059) Yhr116wp [Saccharomyces cerevisiae]
% id cvrg	63	34	34	22		47		42
	34	0 35	6 53	1 43	4	6 39		14
Blast Prob 1.00E-18	9.00E-40 34	0.000000 35 001	5.00E-36 53	8.00E-21 43	1.00E-24	1.00E-26 39	0.00005	0.0002
Blast Score 63	164	49	116	92	113	120	84	46
aat Score 414	505	110	340	615	142	249	89	84
ncbi gi g123338	g3378265	g1730527	g3913983	g3647341	g3668152	g2131257	g1296845	g731704
Database Hit ncbi gi g12333								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos	796-815	453-479	526-552	699-726	757-781	633-660	455-479	459-479
5 pos	29-48	29-52	25-52	39-66	53-72	206-233	32-51	22-46
Contig source ANI61C2070: 1017451	3 ANI61C31:35		5 ANI61C7983: 5841	6 ANI61C7368: 14921	7 ANI61C2088:		9 ANI61C3867: 10451509	0 ANI61C6714: 572872
Seq num Seq id 24008 ENU07802	24009 ENU07803 ANI61C31:35 29-48	24010 ENU07804	24011 ENU07805 ANI61C7983: 25-52 5841	24012 ENU07806 ANI61C7368: 39-66 14921	24013 ENU07807 ANI61C2088: 53-72	24014 ENU07808	24015 ENU07809 ANI61C3867: 32-51	24016 ENU07810 ANIGIC6714: 22-46 572872

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% cvrg Description 55 nuclear protein SNF4 (regulatory protein CAT3); CAT3 protein - yeast (Saccharomyces cerevisiae); (M21760) regulatory protein CAT3 [Saccharomyces cerevisiae]; (M30470) SNF4 protein [Saccharomyces cerevisiae]; (Z72637) ORF YGL115w [Saccharomyces cerevisiae]	"(AL031852) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe]; (AL031856) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces nombe] "	probable sterignatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62); (U34740) putative p450 monooxygenase [Emericella nidulans]	(AF013216) unknown [Myxococcus xanthus]	hypothetical 65.3 KD protein in SUN4-MAS5 intergenic region; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae); (U12141) membrane protein [Saccharomyces cerevisiae]; (Z71341) ORF YNL065w [Saccharomyces cerevisiae]	cytochrome B5	(AF069765) signal recognition particle 72 [Homo sapiens]; (AF077019) signal recognition particle 72 [Homo sapiens]	probable sucrose utilization protein SUC1	(AB003395) ent-Kaurene synthase [Phaeosphaeria sp. L487]
% cvrg	20	26		38	55	04	35	26
% id 58	92 9	32		25	48	5 27	) 29	3 37
Blast Prob % 5.00E-47 58	1.00E-56 56	2.00E-11 32	4.6	3.00E-12 25	6.00E-15 48	3.00E-15 27	1.00E-10 29	2.00E-13 37
Blast Score 96	219	70	31	61	81	83	99	9/
aat Score 472	516	209	100	143	158	251	126	207
ncbi gi g115689	g3738140 516	g2493391	g2384693 100	g1730741 143	g117808	g3243033	g1174472	g2443355
Database Hit ncbi gi g11568								
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP
Primer 3 pos 532-559	438-461		423-450		450-477	800-819		728-754
Primer 5 pos 22-40	26-53		23-42		45-64	28-54		22-46
Seq num Seq id Contig source : 24017 ENU07811 ANI61C2045: ; 6601	24018 ENU07812 ANI61C3092: 26-53 44515044	24019 ENU07813 ANI61C9741: 53566142	24020 ENU07814 ANI61C6714: 23-42 66617031	24021 ENU07815 ANI61C2101: 6701	24022 ENU07816 ANI61C3893: 45-64 16691973	24023 ENU07817 ANI61C9739: 28-54 44572354	24024 ENU07818 ANI61C7925: 40423499	24025 ENU07819 ANI61C6769: 22-46 1062258
Seq num 24017 F	24018 1	24019 1	24020 1	24021	24022	24023	24024 ]	24025

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, ,	(Z97209) ureidoglycolate hydrolase [Schizosaccharomyces pombe]	hypothetical 65.0 KD protein in MET2-SEC2 intergenic region; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae); (Z71551) ORF YNL275w [Saccharomyces cerevisiae]	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum; (M37461) FAS2 protein [Penicillium patulum] "	(AC003952) putative histidine kinase [Arabidopsis thaliana]	(AF016696) peptide synthetase module [Streptomyces fradiae]	DNA polymerase alpha/PRIMASE associated subunit (P86 subunit); probable membrane protein YBL035c-yeast (Saccharomyces cerevisiae); (X74738) ORF YBL0415	[Saccharonnycs cefevisiae], (25) (29) ORF YBL035c [Saccharomyces cerevisiae]; ORF YBL0415 [Saccharomyces cerevisiae]	hypothetical 50.2 KD protein in CPT1-SPC98 intergenic region; probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae); (Z46843) tyrosine phosphatase (putative) [Saccharomyces cerevisiae]; (Z71404) ORF YNL128w [Saccharomyces cerevisiae]	(Y15781) transketolase 1 [Capsicum annuum]
% d cvrg 29	76	26	15			34		32	16
	8.00E-15 32	1.00E-34 48	1.00E-80 52	0.000000	2.00E-21	1.00E-35 39		0.000000 35 06	2.00E-26 58
Blast Score 87	80	146	299	09	102	150		42	118
aat Score 265	137	159	2976	74	82	415		86	312
42	g2239197	g1730641	g119830	g2708752	g2738765	g585063		g1730775 98	g3559814
Database Hit ncbi gi g40386									
Selection Basis LINAP	LINAP	LINAP	LINAP	LINAP	LINAP	LINAP		LINAP	LINAP
Primer 3 pos	455-479	468-495	807-829	420-439	706-731	618-639		472-494	264-283
Primer 5 pos	211-238	37-57	52-71	22-43	101-127	22-42		35-54	24-42
Seq num Seq id Contig source ( 24026 ENU07820 ANI61C2111: 316685	24027 ENU07821 ANI61C3136: 211-238 455-479 328713	24028 ENU07822 ANI61C9770: 37-57 31233644	24029 ENU07823 ANI61C7336: 52-71 13069	24030 ENU07824 ANI61C2130: 22-43 58197	24031 ENU07825 ANI61C3134: 101-127 706-731 20891338	24032 ENU07826 ANI61C9760: 22-42 7411		24033 ENU07827 ANI61C6776: 35-54 14361979	24034 ENU07828 ANI61C3146: 24-42 16032092

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% cvrg Description											
pi %	114, 37, 31, 41, 12,	73	31	24	28	-59, 35"	41	41	25	57,	-63, 10, 08"
Blast Blast Score Prob 1.4E-57	"4.8e-14, 1.9e-37, 4.7e-31, 4.5e-41, 4.6e-13, 3.6e-12, 6.2e-10,	2.2E-73	2.8E-31	2.2E-24	3.4E-28	"1.7e-59 2.2e-35"	2.4E-41	4.2E-41	1.7E-25	"7.3e- 143, 8.3e-57, 1.7e-	"3.8e-63, 7.1e-10, 7.4e-08"
aat Score											
lit ncbi gi 1	4, 8, 6, 6, 1, 8, 1	. <b>.</b> .	L	6	7	20, :6"	91	8	91	.19, 32, 30"	.74, 70, 70"
Database Hit AFUc04191	"AFUC11304 AFUC11498, AFUC11616, AFUC15909, FGRC10768, ECBC16185"	AFUc11953	AFUc10467	AFUc15379	AFUc03772	"AFUc06520, FGRc12926"	AFUc04846	AFUc03198	FGRc09646	"AFUc13219, AFUc19102, CALc06130"	"AFUc12274, AFUc19270, AFUc19270"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
er Primer 3 pos											
Seq Primer num Seq id Contig source 5 pos 24035 ENU07830 ANI61C1460:	24036 ENU07831 ANI61C2191: 60332276	24037 ENU07832 ANI61C1464: 79374	24038 ENU07833 ANI61C1466: 193825	24039 ENU07834 ANI61C1468: 478158	24040 ENU07835 ANI61C1469: 7401360	24041 ENU07836 ANI61C2198: 8789	24042 ENU07837 ANI61C1474: 1420	24043 ENU07838 ANI61C302:2 2751774	24044 ENU07839 ANI61C304:5 59966	24045 ENU07840 ANI61C305:2 799474	24046 ENU07841 ANI61C1027 0:60657449

aat Blast Blast % Score Score Prob % id cvrg Description "1.6e- 111, 6.2e-14,	"4.3e-09, 9.4e-21"	"7.0e-23, 3.3e-23, 3.9e-14, 3.9e-24, 1.9e-13, 3.3e-25, 2.7e-07"	3.9E-33	"4.2e-36, 6.7e-28"	"3.3e-81, 1.6e-08"	8.1E-30	"7.8e-46, 1.3e-45, 1.0e-20, 3.2e-18, 9.6e-14"	1.3E-129	"9.0e-29, 6.1e-39"	6.0e-55
Selection Basis Database Hit ncbi gi GTBX "AFUc01302, AFUc18982, FGRc04116"	GTBX "AFUc05575, AFUc07542"	GTBX "AFUc01701, AFUc09710, AFUc12211, AFUc20787, AFUc21939, Z71256"	GTBX FGRc22675	GTBX "AFUc10211, AFUc15427"	GTBX "AFUc04386, CALc02388"	GTBX AFUc14845	GTBX "AFUc01505, AFUc06388, FGRc05792, FGRc08715, FGRc10632"	GTBX AFUc14473	GTBX "CALc03391, Y13137"	GTBX U00092
Primer Primer Contig source 5 pos 3 pos ANIG1C1027 3:2501270	ANI61C1027 4:28453490	ANI61C1027 5:25514131	ANI61C1027 9:791101	ANI61C1481: 59254	ANI61C1487: 9631571	ANI61C1489: 487281	ANI61C1028 0:1900466	ANI61C1028 2:12071860	ANI61C1028 5:548831	ANI61C1028 7:16842097
Seq num Seq id C 24047 ENU07842 <i>t</i>	24048 ENU07843 ANI61C1027 4:28453490	24049 ENU07844 ANI61C1027 5:25514131	24050 ENU07845 ANI61C1027 9:791101	24051 ENU07846 ANI61C1481: 59254	24052 ENU07847 ANI61C1487: 9631571	24053 ENU07848 ANI61C1489: 487281	24054 ENU07849 ANI61C1028 0:1900466	24055 ENU07850 ANI61C1028 2:12071860	24056 ENU07851 ANI61C1028 5:548831	24057 ENU07852 ANI61C1028 7:16842097

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Seq num Seq id 24058 ENU07853	Contig source ANI61C1493: 1171265	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc19753, FGRc23159"	aat Blast Blast % Score Score Prob % id cvrg "2.0e-25, 7.6e-27"	g Description
24059 ENU07854 ANI61C1495: 294538	ANI61C1495: 294538			GTBX	U00094	1.6e-51	
24060 ENU07855 ANI61C1496: 741115	ANI61C1496: 741115			GTBX	AFUc03226	1.3E-38	
24061 ENU07856 ANI61C320:2 51612	ANI61C320:2 51612			GTBX	AFUc12957	1.1E-40	
24062 ENU07857 ANI61C321:7 2296601	ANI61C321:7 2296601			GTBX	AFUc21833	· 5E-31	
24063 ENU07858 ANI61C322:3 2603635	ANI61C322:3 2603635			GTBX	"AFUc20332, FGRc09045"	"4.5e-25, 5.0e-15"	
24064 ENU07859 ANI61C327:4 0034	ANI61C327:4 0034			GTBX	FGRc11552	3E-22	
24065 ENU07860 ANI61C1029 6:266918	ANI61C1029 6:266918			GTBX	"AFUc15183, CALc05935"	"1.6e-85, 5.4e- 26?"	
24066 ENU07861 ANI61C1 6:11566	ANI61C1029 6:115661224			GTBX	AFUc15911	7E-93	
24067 ENU07862 ANI61C1029	ANI61C1029 7:231444			GTBX	AFUc15769	9.4E-113	
24068 ENU07863 ANI61C1029 9:15373212	ANI61C1029 9:15373212			GTBX	"AFUc21263, FGRc09112"	"3.8e-55, 6.6e-63"	
24069 ENU07864 ANI61C1029 9:48923860	ANI61C1029 9:48923860			GTBX	AFUc12138	5.7E-25	
24070 ENU07865 ANI61C1029 9:59286774	ANI61C1029 9:59286774			GTBX	AFUc03113	5.7E-64	
24071 ENU07866 ANI61C1:30 683	ANI61C1:30 683			GTBX	AFUc09360	4.1E-27	

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24072 ENU07867 ANI61C1:104	Selection Basis GTBX	Database Hit ncbi gi AFUc18004	aat Blast Blast Score Score Prob 7.5E-30	% id cvrg Description
24073 ENU07868 ANI61C2:458 5	GTBX	"AFUc04176, FGRc07928"	"3.7e-38, 1.7e-22"	
24074 ENU07869 ANI61C330:2 1121395	GTBX	AFUc02133	2.9E-65	
24075 ENU07870 ANI61C333:6 49911	GTBX	AFUc06176	7.7E-23	
24076 ENU07871 ANI61C340:9 66691	GTBX	AFUc04374	1.7E-27	
24077 ENU07872 ANI61C343:6 7613	GTBX	AFUc12179	7E-45	
24078 ENU07873 ANI61C345:2 8531498	GTBX	AFUc12264	1.2E-94	
24079 ENU07874 ANI61C352:1 134111766	GTBX	"AFUc12377, X59720"	"1.8e-70, 2.1e-12"	
24080 ENU07875 ANI61C352:1 290412374	GTBX	AFUc12377	2E-59	
24081 ENU07876 ANI61C362:1 701977	GTBX	"AFUc12101, AFUc14601, FGRc23569"	"6.3e- 111, 9.1e-18, 2.5e-38"	
24082 ENU07877 ANI61C7202: 1145858	GTBX	"AFUc05840, AFUc05840, CAL c06220"	"4.0e-26, 7.6e-12, 7.2e-58"	
24083 ENU07878 ANIGIC7204: 12881623	GTBX	AFUc14370	7.4E-25	
24084 ENU07879 ANI61C373:4 8451	GTBX	AFUc17629	5.7E-30	
24085 ENU07880 ANI61C379:4 0166	GTBX	Y13135	3.8e-21	

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aat Blast Blast % Score Score Prob % id cvrg Description "9.7e-37, 2.3e-30"	"2.4e-12, 1.1e-35"	8.5E-76	"3.1e-95, 4.2e-07"	"2.2e-24, 2.1e-14, 3.0e-17"	"2.5e- 164, 9.5e-14"	2.9E-60	"2.6e-52, 5.2e- 157, 1 0e-21"	"6.8e-44, 4.9e-23"	3.4E-43	"3.6e-82, 4.6e-80, 2.3e-35"	"1.2e-76, 1.0e-07, 4.8e-25,	3.8E-27
Selection Basis Database Hit ncbi gi GTBX "FGRc17352, U00092"	GTBX "AFUc06725, AFUc09341"	GTBX AFUc13794	GTBX "AFUc11055, FGRc22632"	GTBX "AFUc00779, FGRc05727, FGRc22503"	GTBX "AFUc12900, FGRc14925"	GTBX AFUc01942	GTBX "AFUc05806, AFUc12778, AFUc19750"	GTBX "AFUc16901, FGRc10006"	GTBX AFUc03224	GTBX "AFUc08318, AFUc08318, FGRc09465"	GTBX "AFUc04514, AFUc13919, CALC05514,	GTBX AFUc16862
Seq Primer Primer S num Seq id Contig source 5 pos 3 pos B 24100 ENU07895 ANIGLC7249: G	24101 ENU07896 ANI61C6521: G	24102 ENU07897 ANI61C7251: G 60910	24103 ENU07898 ANI61C7252: G 78543	24104 ENU07899 ANI61C6526: 44723329	24105 ENU07900 ANI61C6527: G 61586573	24106 ENU07901 ANI61C6532: C	24107 ENU07902 ANI61C6532: C 39566787	24108 ENU07903 ANI61C6535: C 41905827	24109 ENU07904 ANI61C6535: C	24110 ENU07905 ANI61C5807: 6701293	24111 ENU07906 ANI61C5808: C 5141299	24112 ENU07907 ANI61C5809: C 2846

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24113 ENU07908 ANI61C5810: 81947	Selection Basis GTBX	Database Hit ncbi gi "AFUc08467, CALc05923"	aat Blast Blast Score Score Prob "4.4e-09 8.3e-56"	% % id cvrg Description
24114 ENU07909 ANI61C6540: 31193417	GTBX	AFUc08906	9E-44	
24115 ENU07910 ANI61C5813: 4601074	GTBX	AFUc12201	7.9E-95	
24116 ENU07911 ANI61C7273: 9602083	GTBX	AFUc10281	1.1E-47	
24117 ENU07912 ANI61C7274: 1136206	GTBX	AFUc03210	2.9E-57	
24118 ENU07913 ANI61C7276: 35274341	GTBX	"AFUc01802, FGRc10582"	"1.6e-22, 1.3e-15"	
24119 ENU07914 ANI61S207:5 43121	GTBX	AFUc07853	3.8E-25	
24120 ENU07915 ANI61C7280: 3351938	GTBX	"FGRc08244, FGRc16187"	"1.3e-71, 2.0e-46"	
24121 ENU07916 ANI61C6552: 31344669	GTBX	"AFUc13978, AFUc16716, AFUc19617, FGRc1557"	"1.1e-31, 1.4e-29, 2.0e-44, 6.2e-18"	
24122 ENU07917 ANI61C6553: 38694420	GTBX	AFUC11116	5.8E-30	
24123 ENU07918 ANI61C6556: 44197	GTBX	AFUc13317	1.2E-36	
24124 ENU07919 ANI61C7285: 9161315	GTBX	FGRc02595	1.9E-36	
24125 ENU07920 ANI61C7285: 79008248	GTBX	AFUc15172	4.4E-69	
24126 ENU07921 ANI61C5829: 736359	GTBX	AFUc08971	4.2E-34	

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24127 ENU07922 ANI61S219:4 849	Selection Basis GTBX	Database Hit ncbi gi AFUc08358	aat Blast Blast Score Score Prob % id 1.5E-60	% id cvrg Description
24128 ENU07923 ANI61C5831: 90318	GTBX	AFUc14499	6.3E-77	
24129 ENU07924 ANI61C7290: 909336	GTBX	Y13134	3.0e-28	
24130 ENU07925 ANI61C6562: 102089	GTBX	"AFUc01328, AFUc04061"	"6.1e-55, 3.1e-53"	
24131 ENU07926 ANI61C5834: 5361960	GTBX	CALc03151	8.9E-171	
24132 ENU07927 ANI61C5835: 1327116	GTBX	"AFUc02187, AFUc12580, AFIL:16794"	"1.4e-14, 1.9e-07, 4.2e-61"	
24133 ENU07928 ANI61C6564: 16965	GTBX	"AFUc16593, FGRc03157"	"4.2e-43, 1.2e-11"	
24134 ENU07929 ANI61C5836: 6935	GTBX	"CALc04906, FGRc04099"	"2.4e-48, 8.5e-59"	
24135 ENU07930 ANI61C5837: 3117648	GTBX	AFUc14040	8.4E-26	
24136 ENU07931 ANI61C7298: 5928	GTBX	CALc06027	3E-39	
24137 ENU07932 ANI61C6570: 951739	GTBX	CALc06157	1.4E-65	
24138 ENU07933 ANI61C6579: 931141	GTBX	"AFUc02825, AFUc16044"	"9.5e-21, 9.7e-09"	
24139 ENU07934 ANI61C5852: 88835	GTBX	CALc05688	3.7E-57	
24140 ENU07935 ANI61C5852: 22811223	GTBX	"AFUc07544, AFUc08833"	"7.4e-09, 2.7e-29"	

### center of the second

Seq Contig source 5 pos 10071811   24141 ENU07936 ANI61C6585: 10071811   24142 ENU07937 ANI61C6588: 180414   8921140   24144 ENU07940 ANI61C6598: 15732608   24145 ENU07941 ANI61S8:287. 47   24146 ENU07942 ANI61C5885: 3611250   24149 ENU07944 ANI61C5886: 756.40   24150 ENU07945 ANI61C2202: 43360   24151 ENU07946 ANI61C2202: 54616   24152 ENU07948 ANI61C2202: 7371023   24153 ENU07948 ANI61C2202: 7371023   24153 ENU07948 ANI61C2209: 128864	3 pos	Selection Basis GTBX GTBX GTBX GTBX GTBX GTBX GTBX GTBX	Database Hit ncbi gi "AFUc10318, AFUc15156" "AFUc05311, AFUc08311" "AFUc08190, AFUc11152, AFUc11152, AFUc11152, AFUc10830, FGRc04488" AFUc04879 AFUc19850 AFUc19850 AFUc105111 AFUc10677, Y13136" "AFUc17374, AFUc17374, AFUc17374,	Score Score Prob % id cvrg "4.9e-73, "1.7e-72" "1.7e-47, "1.7e-47, "1.2e-09, 2.1e-62, 3.6e-10, 1.1e-08" "1.1e-08" "1.1e-94 3.4e-94 3.4e-95 3.2e-36 3.2e-39 3.2e-39	% id cvrg Description .
24154 ENU07949 ANI61C1100 0:82629041		GTBX	AFUc14297	3.3E-45	

### nouceel leading

Seq num Seq id 24155 ENU07950	Contig source ANI61C1100 4:19541302	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc14982	aat Blast Blast Score Score Prob IE-161	% id cvrg Description
24156 ENU07951 ANI61C2214: 16951099	ANI61C2214: 16951099			GTBX	AFUc10709	1.3E-47	
24157 ENU07952 ANI61C2216: 541022	ANI61C2216: 541022			GTBX	Z71256	9.0e-15	
24158 ENU07953 ANI61C1101 0:12432169	ANT61C1101 0:12432169			GTBX	"AFUc14408, FGRc07288"	"4.0e-33, 2.4e-38"	
24159 ENU07954 ANI61C2220: 29773	ANI61C2220: 29773			GTBX	AFUc02313	8.5E-22	
24160 ENU07955 ANI61C1102 3:791083	ANI61C1102 3:791083			GTBX	"AFUc06153, AFUc21355, FGP-08305"	"3.7e-61, 9.8e-54, 4.2e-07"	
24161 ENU07956 ANI61C2235: 19661466	ANI61C2235: 19661466			GTBX	AFUc06983	6.5E-57	
24162 ENU07957 ANI61C1103 0:3002243	ANI61C1103 0:3002243			GTBX	"AFUc15517, AFUc20784, EGB c15017"	"2.6e-20, 4.8e-15,	
24163 ENU07958 ANI61C1103 0:84099713	ANI61C1103 0:84099713			GTBX	"AFUc06388, FGRc05792"	"1.0e-22, "1.0e-22, 8.0e-25"	
24164 ENU07959 ANI61C1103 1:16552023	ANI61C1103 1:16552023			GTBX	AFUc13932	2.9E-51	
24165 ENU07960 ANI61C1103 2:49748	ANI61C1103 2:49748			GTBX	AFUc11402	2.7E-50	
24166 ENU07961 ANI61C1030 4:273800	ANI61C1030 4:273800			GTBX	AFUc15094	5.6E-72	
24167 ENU07962 ANI61C1030 6:61314	ANI61C1030 6:61314			GTBX	AFUc13032	4.4E-37	
24168 ENU07963 ANI61C1103 7:57756531	ANI61C1103 7:57756531			GTBX	AFUc07195	7E-57	

Seq num Seq id 24169 ENU07964	Contig source ANI61C1103 8:142251277	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc09489, FGRc09616"	aat Blast H Score Score F	Blast Prob % i "9.0e-26, 3.6e-17"	% id cvrg Description
0 24170 ENU07965 ANI61S1 92435	0 ANI61S1346: 92435			GTBX	AFUc02348		1.4E-44	
24171 ENU07966 ANI61C1 3781139	ANI61C1511: 3781139			GTBX	U00094	41	5.2e-38	
24172 ENU07967 ANI61C2242: 24061912	ANI61C2242: 24061912			GTBX	AFUc03452	~	8.1E-49	
24173 ENU07968 ANI61C1 220815	ANI61C1514: 220815			GTBX	AFUc15554		1.7E-79	
24174 ENU07969 ANI61C1 1333817	ANI61C1518: 1333817			GTBX	"AFUc13493, FGRc25564"	. ,	"6.5e-23, 4.9e-25"	
24175 ENU07970 ANI61C2249: 68817	ANI61C2249: 68817			GTBX	AFUc08878	.,	3.5E-79	
24176 ENU07971	ANI61C1031 0:133571			GTBX	AFUc09721		3.6E-27	
24177 ENU07972 ANI61C1104 0:20022735	ANI61C1104 0:20022735			GTBX	AFUc09896		3.5E-52	
24178 ENU07973 ANI61C1 1:85119	ANI61C1104 1:8511973			GTBX	AFUc10517		2.5E-94	
24179 ENU07974 ANI61C1 3:38529	ANI61C1031 3:38529			GTBX	FGRc07645		1.9E-21	
24180 ENU07975 ANI61C1104 5:39677	ANI61C1104 5:39677			GTBX	U00094		6.2e-38	
24181 ENU07976 ANI61C1104 6:529740	ANI61C1104 6:529740			GTBX	AFUc10641		6.5E-39	
24182 ENU07977 ANI61C1521: 34572237	ANI61C1521: 34572237			GTBX	AFUc12939		2.7E-101	

### celen celenation

Sec		Primer	Primer	Selection		aat Blast	Blast	%
24183 ENU07978 ANI61C1525: 1163813	Contig source ANI61C1525: 1163813	5 pos	3 pos	Basis GTBX	Database Hit ncbi gi FGRc04252	ភ	23	% id cvrg Description
24184 ENU07979 ANI61C2256: 1738606	ANI61C2256: 1738606			GTBX	"AFUc03478, AFUc06959, FGRc11107"		"5.3e-61, 1.4e-13, 1.6e-68"	
24185 ENU07980 ANI61C1032 4:14562640	ANI61C1032 4:14562640			GTBX	AFUc06432		5.6E-40	
24186 ENU07981 ANI61C1032 4:66837378	ANI61C1032 4:66837378			GTBX	AFUc03858		1.8E-26	
24187 ENU07982 ANI61C1105 7:8543	ANI61C1105 7:8543			GTBX	AFUc15404		1.2E-104	
24188 ENU07983 ANI61C1105 8:12353139	ANI61C1105 8:12353139			GTBX	"AFUc10292, CALc04898"		"1.7e- 140, 3.7e-15"	
24189 ENU07984 ANI61C2264: 819487	ANI61C2264: 819487			GTBX	AFUc14213		4.3E-22	
24190 ENU07985 ANI61C2266: 6781117	ANI61C2266: 6781117			GTBX	AFUc09002		2.9E-60	
24191 ENU07986 ANI61C1538: 15272143	ANI61C1538: 15272143			GTBX	FGRc13890		2.3E-55	
24192 ENU07987 ANI61C1106 5:130825	ANI61C1106 5:130825			GTBX	"AFUc01902, CALc06224"		"2.0e-49, 2.4e-36"	
24193 ENU07988 ANI61C1033 8:10681298	ANI61C1033 8:10681298			GTBX	AFUc15802		5.7E-81	
24194 ENU07989 ANI61C2274: 104352	ANI61C2274: 104352			GTBX	FGRc17081		5.7E-24	
24195 ENU07990 ANI61C2279: 94735	ANI61C2279: 94735			GTBX	AFUc12999		3.7E-57	
24196 ENU07991 ANI61C1107 3:108259957	ANI61C1107 3:108259952			GTBX	AFUc08864		1.6E-40	

Seq         Contig source         Frimer         Primer           num         Seq id         Contig source         5 pos         3 pos           24197 ENU07992 ANIGICI107         6:148474         5:148474           24198 ENU07993 ANIGICI107         6:73540         5:73540           24200 ENU07994 ANIGICI554:         1454495         5052120           24201 ENU07996 ANIGICI556:         5052120         5052120           24202 ENU07997 ANIGICI557:         83778816         24203           24203 ENU07999 ANIGIC2286:         63469         2411075           24204 ENU08000 ANIGICI558:         2411075           24205 ENU08001 ANIGICI108         2.2355           24207 ENU08002 ANIGICI103         27413           24208 ENU08003 ANIGICI035         4:586266	Selection Basis GTBX GTBX GTBX GTBX GTBX GTBX GTBX GTBX	Database Hit ncbi gi AFUc15190 FGRc11607 "AFUc22243, Z71256" "AFUc16791, CALc05767" "FGRc16102, U00091" "AFUc10195, Y13137" AFUc19350 AFUc19350 AFUc11431 AFUc00871	aat Blast Blast Score Score Prob 5.2E-32 9.9E-62 3.3e-65" "1.1e-89, 9.6e-28" "3.0e-18, 6.1e-13" "2.6e-29, 3.3e-19" 1.8E-29 1.8E-38 1.8E-38	% id cvrg Description
24209 ENU08004 ANI61C1561: 6331091	GTBX	"FGRc12428, FGRc23250"	"6.2e-17, 1.3e-26"	
24210 ENU08005 ANI61C1563: 759984	GTBX	AFUc12486	1.4E-59	

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24211 ENU08006 ANI61C1564: 4251061	Selection Basis GTBX	Database Hit ncbi gi "AFUc03100, AFUc08293"	aat Blast 8% Score Score Prob % id cvrg Description "1.6e-71, 1.0e-71"
24212 ENU08007 ANI61C1566: 19211217	GTBX	AFUc06344	1.5E-31
24213 ENU08008 ANI61C1036 2:7061638	GTBX	AFUc05986	2.IE-64
24214 ENU08009 ANI61C1036 3:84749	GTBX	AFUc14403	5.9E-76
24215 ENU08010 ANI61C1109 3:666283	GTBX	AFUc02155	7.1E-43
24216 ENU08011 ANI61C1109 8:57746408	GTBX	"AFUc02174, AFUc07223"	"3.6e-30, 1.4e-64"
24217 ENU08012 ANI61C1571: 1373765	GTBX	AFUc09738	2.6E-96
24218 ENU08013 ANI61C1572: 1528	GTBX	AFUc12035	6.1E-42
24219 ENU08014 ANI61C1575: 5381212	GTBX	AFUc17343	5.4E-29
24220 ENU08015 ANI61C404:2 381.3391	GTBX	AFUc10663	1.6E-86
24221 ENU08016 ANI61C404:5 5434664	GTBX	AFUc05891	3.5E-65
24222 ENU08017 ANI61C409:1 65041	GTBX	"AFUc07919, AFUc13887, AFUc14801, AFUc20578"	"3.7e-46, 4.4e-36, 1.0e-15, 2.9e-59"
24223 ENU08018 ANI61C1580: 5321125	GTBX	AFUc13632	1.9E-52
24224 ENU08019 ANI61C1582: 9093	GTBX	Z71257	2.9E-22

Blast Blast % Score Prob % id cvrg Description 3.2E-39	4.2E-32	1.1E-49	8.7E-94	1.9E-37	"1.9e-45, 5.7e-53"	4.3E-35	"1.1e-28, 2.2e-12, 1.3e-46"	"5.1e-14, 1.1e-15, 1.4e-14, 1.3e-	6E-60	"2.8e-11, 6.6e-93"	8.2E-24	5.3E-40
aat ncbi gi Score												
n Database Hit AFUc13343	AFUc16966	FGRc26357	AFUc15000	AFUc14146	"AFUc04379, AFUc12739"	AFUc16619	"AFUc06152, AFUc17696, CALc05205"	"AFUc07197, AFUc11134, AFUc11728, AFUc12186"	AFUc01048	"AFUc02858, U00092"	AFUc19180	AFUc13623
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos												2
Seq num Seq id Contig source 5 p 24225 ENU08020 ANI61C1586: 7871352	24226 ENU08021 ANI61C1038 0:31893954	24227 ENU08022 ANI61C419:2 8469	24228 ENU08023 ANI61C1038 4:6822	24229 ENU08024 ANI61C1038 6:4286	24230 ENU08025 ANI61C1038 7:32704847	24231 ENU08026 ANI61C1598: 47911	24232 ENU08027 ANI61C1039 7:1214133	24233 ENU08028 ANI61C438:2 608906	24234 ENU08029 ANI61C439:9 1249705	24235 ENU08030 ANI61C8000: 9942	24236 ENU08031 ANI61C8004: 6083	24237 ENU08032 ANI61C8006: 5141077

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Seq num Seq id Contig 24238 ENU08033 ANI61 44639	source C440:3	Primer 15 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc17537	aat Blast Score Score	Blast Prob 3.9E-64	% id cvrg Description
24239 ENU08034 ANI61C442:5 56131	ANI61C442:5 56131			GTBX	AFUc21017		6.4E-22	
24240 ENU08035 ANI61C445:7 161232	ANI61C445:7 161232			GTBX	GY13139		5.9e-57	
24241 ENU08036 ANI61C449:2 661975	ANI61C449:2 661975			GTBX	AFUc15617		1.4E-206	
24242 ENU08037 ANI61C8012: 1970190	ANI61C8012: 1970190			GTBX	AFUc15379		5.1E-111	
24243 ENU08038 ANI61C8013. 18513360	ANI61C8013: 18513360			GTBX	"AFUc07084, AFUc22432, CALc06078, V13135"		"4.8e-66, 2.1e-41, 1.1e-54, 5.7e-37"	
24244 ENU08039 ANI61C8020: 5382	ANI61C8020: 5382			GTBX	AFUc13797		2.5E-36	
24245 ENU08040 ANI61C8021: 35452350	ANI61C8021: 35452350			GTBX	AFUc13604		6.6E-63	
24246 ENU08041 ANI61C8026: 381772	ANI61C8026: 381772			GTBX	"AFUc15772, AFUc21150, FGRc16885"		"4.9e- 143, 2.0e-13,	
24247 ENU08042 ANI61C8029: 16570	ANI61C8029: 16570			GTBX	AFUc21824		1.3E-47	
24248 ENU08043 ANI61C467:5 3716057	ANI61C467:5 3716057			GTBX	AFUc04398		1.6E-38	
24249 ENU08044 ANI61C8031: 823117	ANI61C8031: 823117			GTBX	AFUc11877		2.7E-59	
24250 ENU08045 ANI61C7308: 36415	ANI61C7308: 36415			GTBX	AFUc00888		4.1E-24	

Blast Blast % Score Prob % id cvrg Description 1.5E-52	"5.4e-16, 5.2e-55"	5E-46	"2.1e-43, 2.9e-37"	"8.6e- 115, 1.2e-67,	5.4E-21	"6.8e-21, 1.2e-09"	1.9E-80	"1.4e-61, 3.0e-62"	7E-56	"2.8e-71, 6.0e-34, 7.0s.55"	1.7E-21	"5.7e-57, 4.0e-21, 5.0e-19, 6.6e-14"
aat Score												
Database Hit ncbi gi AFUc15892	"AFUc04986, AFUc09264"	AFUc14880	"AFUc12313, AFUc19899"	"AFUc11411, CALc06214, Y13135"	AFUc15695	"AFUc18123, Y13139"	AFUc13648	"CALc04459, CALc04459"	AFUc19691	"AFUc00069, AFUc16115,	AFUc10161	"AFUc11740, AFUc12687, AFUc14731, FGRc23552"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24251 ENU08046 ANI61C477:6 301	24252 ENU08047 ANI61C7311: 163582	24253 ENU08048 ANI61C8044: 3261058	24254 ENU08049 ANI61C7315: 18413604	24255 ENU08050 ANI61C7317: 166656	24256 ENU08051 ANI61C8047: 52424733	24257 ENU08052 ANI61C7318: 6551047	24258 ENU08053 ANI61C489:4 573	24259 ENU08054 ANI61C8051: 1747518	24260 ENU08055 ANI61C7323: 785241	24261 ENU08056 ANI61C8052: 7332502	24262 ENU08057 ANI61C8053: 610182	24263 ENU08058 ANI61C8055: 2135174

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Seq num Seq id Contig source 24264 ENU08059 ANI61C8057. 52420		Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit nc AFUc08475	aat ncbi gi Score	Blast re Score	Blast Prob 9 2E-49	% id cvrg I	Description
24265 ENU08060 ANI61C7329: 5941704	ANI61C7329: 5941704			GTBX	"AFUc01746, AFUc02096"			"1.2e-27, 3.5e-52"		
24266 ENU08061 ANI61C492:5 7884	ANI61C492:5 7884			GTBX	AFUc13259			3.6E-135		
24267 ENU08062 ANI61C499:1 160732	ANI61C499:1 160732			GTBX	AFUc09357			1.1E-68		
24268 ENU08063 ANI61C7330: 1432372	ANI61C7330: 1432372			GTBX	"AFUC13887, AFUC14801, FGRc09062, FGRC10889,			"2.5e-43, 1.3e-13, 1.6e-45, 5.2e-99,		
24269 ENU08064 ANI61C7330: 33674124	ANI61C7330: 33674124			GTBX	FGRC11979" "AFUc05528, FGRc11979"			1.3e-10 "6.7e-27, 3.8e-13"		
24270 ENU08065 ANI61C7331: 40112258	ANI61C7331: 40112258			GTBX	"AFUc03996, AFUc06614, AFUc15699, AFIC15879"			"1.6e-21, 3.9e-15, 3.4e-19,		
24271 ENU08066 ANI61C6607: 14092016	ANI61C6607: 14092016			GTBX	"AFUc10110, AFUc19217"			"5.5e-22, 1.4e-48"		
24272 ENU08067 ANI61C8066: 8661393	ANI61C8066: 8661393			GTBX	"AFUc11731, CALc05890"			"6.5e- 121, 3.7e-		
24273 ENU08068 ANI61C7340: 4507	ANI61C7340: 4507			GTBX	Y13134			9.1e-28		
24274 ENU08069 ANI61C6611: 98870	ANI61C6611: 98870			GTBX	AFUc07093			4.5E-60		
24275 ENU08070 ANI61C8071: 51613	ANI61C8071: 51613			GTBX	AFUc09728			1.8E-53		

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Seq         Primer         Primer           num         Seq id         Contig source         5 pos         3 pos           24276         ENU08071         ANI61C6614:         1400.874         3 pos           24277         ENU08072         ANI61C8074:         5126.4678         5126.4678           24278         ENU08073         ANI61C6616:         377.1089           24279         ENU08074         ANI61C6617:         4827.5366           24280         ENU08075         ANI61C8082:         1136.2144           24281         ENU08076         ANI61C6626:         6507.7319           24282         ENU08078         ANI61C6626:         6507.7319           24284         ENU08079         ANI61C7356:         585838           24284         ENU08080         ANI61C8087:         24241939	Selection Basis GTBX GTBX GTBX GTBX GTBX GTBX GTBX GTBX	Database Hit ncbi gi AFUc15221 AFUc12456 "AFUc05353, AFUc19936" Z47047 AFUc15770 AFUc10550 AFUc03450 "CALc06084, Y13137" AFUc07211	aat       Blast       %         Score       Prob       % id cvrg       Description         1.2E-142       4 id cvrg       Description         2.7E-29       1.7e-54, 4.0e-12"       1.6e-125         1.6E-22       1.6E-22         2.5E-151       2.5E-151         3.9E-50       3.9E-50         8.3e-235"       4.7E-51
24286 ENU08081 ANI61C5902: 1004261	GTBX	AFUc12988	3.5E-72
24287 ENU08082 ANI61C8090: 55756094	GTBX	FGRc12352	1E-36
24288 ENU08083 ANI61C7361: 15672745	GTBX	AFUc09895	6.4E-117
24289 ENU08084 ANI61C5903: 811368	GTBX	AFUc15950	2.6E-157

### ceceo centro

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24290 ENU08085 ANI61C5904:	Selection Basis GTBX	Database Hit ncbi gi "AFUc00773, AFUc11153"	aat Blast B Score Score P	Blast % Prob % id cvrg Description "7.1e-16, 1.9e-29"	
24291 ENU08086 ANI61C6635: 944282	GTBX	AFUc02614	δ.	5.8E-36	
24292 ENU08087 ANI61C7364: 11682132	GTBX	"AFUc01872, FGRc01926"	: 1 6	"1.0e- 136, 2.4e-24"	
24293 ENU08088 ANI61C5907: 1099443	GTBX	AFUc02783	1 6	2.1E-34	
24294 ENU08089 ANI61C6639: 3067	GTBX	AFUc10259	3	3.7E-24	
24295 ENU08090 ANI61C5910: 53116464	GTBX	AFUc09815	2	2.6E-69	
24296 ENU08091 ANI61C7370: 3691672	GTBX	AFUc10420	ν,	5E-119	
24297 ENU08092 ANI61C5913: 4891	GTBX	"FGRc02041, U00092"	: 0	"6.1e-12, 6.1e-12"	
24298 ENU08093 ANI61C6644: 1478646	GTBX	"AFUc06809, AFUc15344"	: 4	"4.6e-09, 4.4e-98"	
24299 ENU08094 ANI61C5918: 49918	GTBX	FGRc07459	9	6E-57	
24300 ENU08095 ANI61C6649: 10572094	GTBX	AFUc15961	2	2.5E-39	
24301 ENU08096 ANI61C7379: 96228	GTBX	AFUc08907	<b>T</b>	1.2E-21	
24302 ENU08097 ANI61C5922: 1491291	GTBX	"CALc06174, FGRc08383"	: 4	"4.5e-31, 4.8e-31"	
24303 ENU08098 ANI61C7381: 3001060	GTBX	"AFUc10566, AFUc10566"	: 0	"3.6e-30, 9.6e-41"	

### Correct Crance

Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc09205	aat Blast Score Score		% % id cvrg Description
24305 ENU08100 ANI61C7387: 5753		GIBX	FGRC10619		4./E-31	
24306 ENU08101 ANI61C7387: 12791652		GTBX	"AFUc13408, AFUc21306"		"5.7e-19, 1.5e-31"	
24307 ENU08102 ANI61C7389: 132660		GTBX	CALc05599		4.8E-124	
24308 ENU08103 ANI61C5930: 38765599		GTBX	"AFUc13125, AFUc17372"		"4.4e- 183, 1.6e-68"	
24309 ENU08104 ANI61C6660: 2123319		GTBX	"AFUc00228, AFUc00481, AFUc02234"		"5.3e-27, 1.0e-27, 9.8e-33"	
24310 ENU08105 ANI61C7390: 15882441		GTBX	Y13139		1.0e-127	
24311 ENU08106 ANI61C6661: 32265249		GTBX	"AFUc12095, FGRc15027"		"2.5e- 198, 4.1e-29"	
24312 ENU08107 ANI61C6662: 50345514		GTBX	AFUc09341		2.9E-28	
24313 ENU08108 ANI61C7393: 703293		GTBX	AFUc15863		2.6E-52	
24314 ENU08109 ANI61C5938: 1981256		GTBX	AFUc12786		3.3E-79	
24315 ENU08110 ANI61C6670: 12771597		GTBX	AFUc00716		1.4E-36	
24316 ENU08111 ANI61C5943: 62393		GTBX	AFUc15520		1.4E-45	
24317 ENU08112 ANI61C6675: 830254		GTBX	CALc04506		7E-39	

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24318 ENU08113 ANI61C5946:	Selection Basis GTBX	Database Hit ncbi gi AFUc13556	aat Blast Blast % Score Score Prob % id c 1.7E-75	% cvrg Description
24319 ENU08114 ANI61C5952: 52028	GTBX	AFUc17155	3.9E-41	
24320 ENU08115 ANI61C5954: 551083	GTBX	"AFUc03799, AFUc10276"	"3.7e-57, 7.3e-09"	
24321 ENU08116 ANI61C6685: 43903	GTBX	"CALc04792, FGRc09020, U00093"	"2.4e-53, 2.0e-32, 7.8e-49"	
24322 ENU08117 ANI61C5957: 16631999	GTBX	AFUc02793	2.2E-30	
24323 ENU08118 ANI61C6686: 42515701	GTBX	AFUc15881	6.9E-80	
24324 ENU08119 ANI61C5961: 1203511	GTBX	AFUc01030	1.1E-38	
24325 ENU08120 ANI61C5964: 1000.1293	GTBX	AFUc15826	1.8E-25	
24326 ENU08121 ANI61C5966: 658980	GTBX	AFUc14716	8.1E-39	
24327 ENU08122 ANI61C5968: 1055834	GTBX	Z71256	1.4e-23	
24328 ENU08123 ANI61C5975: 178611	GTBX	AFUc02362	1.6E-60	
24329 ENU08124 ANI61C5976: 150586	GTBX	"AFUc15353, CALc06066, FGRc02066"	"8.2e-52, 6.3e-34, 5.0e-73"	
24330 ENU08125 ANI61S2111: 116469	GTBX	FGRc08800	3.9E-32	
24331 ENU08126 ANI61C5984: 211731	GTBX	AFUc15082	4.1E-55	

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Seq num Seq id 24332 ENU08127	Contig source ANI61C5988: 1524225	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc15870, AFUc18615"	aat Blast Score Score	Blast Prob " "1.1e-51, 1.5e-32"	% id cvrg Description	_
24333 ENU08128 ANI61C3014: 1868825	ANI61C3014: 1868825			GTBX	AFUc12007		3.5E-33		
24334 ENU08129 ANI61C3015: 3841558	ANI61C3015: 3841558			GTBX	"AFUc06441, AFUc18928, FGRc12021, EGRc13093"		"1.4e-23, 2.4e-39, 1.4e-23, 4 5e-17"		
24335 ENU08130 ANI61C5995: 1002463	ANI61C5995: 1002463			GTBX	AFUC15651, AFUC15651"		"1.3e-66, 4.5e-89"		
24336 ENU08131 ANI61S 94537	ANI61S2128: 94537			GTBX	AFUc07714		1.3E-44		
24337 ENU08132 ANI61C3022: 992720	ANI61C3022: 992720			GTBX	AFUc07125		7E-30		
24338 ENU08133 ANI61S 44472	ANI61S2133: 44472			GTBX	AFUc22602		1.6E-46		
24339 ENU08134 ANI61C2304: 560132	. ANI61C2304: 560132			GTBX	AFUc07438		1.3E-32		
24340 ENU08135 ANI61C3035: 910296	ANI61C3035: 910296			GTBX	"AFUc11981, FGRc10039"		"6.2e-40, 1.6e-09"		
24341 ENU08136 ANI61C3037: 5797	5797			GTBX	AFUc09927		7.5E-56		
24342 ENU08137 ANI61C2309: 974363	, ANI61C2309: 974363			GTBX	"AFUc03406, AFUc05614, AFUc08898, CAL <sub>C</sub> 05491"		"2.9e-54, 5.7e-54, 1.4e-19, 8.4e-09"		
24343 ENU08138 ANI61C3039. 68847	3 ANI61C3039: 68847			GTBX	CALc04805		2E-93		
24344 ENU08139 ANI61C11110 4:37772731	ANI61C1110 4:37772731			GTBX	AFUc12784		1.3E-86		

# operation of the contraction of

aat Blast Blast % Score Score Prob % id cvrg Description 6.1E-35	1.3E-29	1E-49	3.2E-63	3.6E-39	7.9E-61	"9.5e- 112, 1 7e-33"	7.8E-50	"3.8e-21, 8.0e- 195, 6.4e-24"	"1.6e-07, 9.4e-11, 1.5e-25"	2.7E-24	7.7e-28	"9.8e-76, 1.5e-39"	9.5E-26
ncbi gi								-^ -	<b>-</b> •			<b>~</b> ^-	
Database Hit ncbi gi AFUc15701	AFUc09253	AFUc12154	AFUc07159	FGRc02484	AFUc02336	"AFUc12924 FGRc04111"	AFUc22220	"AFUc00609 AFUc14117, CALc02486"	"AFUc06449, AFUc07501, FGR-07589"	AFUC13156	Y13139	"AFUc01410, CALc06209"	CALc06229
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 24345 ENU08140 ANI61S2144: 27416	24346 ENU08141 ANI61C1110 8:16982135	24347 ENU08142 ANI61C2315: 1253672	24348 ENU08143 ANI61C2318: 4731164	24349 ENU08144 ANI61C3049: 13952904	24350 ENU08145 ANI61S2150: 37833	24351 ENU08146 ANI61C3050: 6252162	24352 ENU08147 ANI61C2321: 1194529	24353 ENU08148 ANI61C3053: 2266185	24354 ENU08149 ANI61C3054: 7472100	24355 ENU08150 ANI61C2325: 74735	24356 ENU08151 ANI61C3057: 21530	24357 ENU08152 ANI61C1112 0:6934	24358 ENU08153 ANI61C1112 5:508269

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24359 ENU08154 ANI61C1112 8:31944053	mer Selection os Basis GTBX	on Database Hit ncbi gi "AFUc09503, CALc05722"	aat Blast Blast Score Score Prob "1.9e-64, 2.7e-76"	% % id cvrg Description
24360 ENU08155 ANI61S1437: 98399	GTBX	"AFUc13604, AFUc15296"	"4.7e-25, 3.3e-21"	
24361 ENU08156 ANI61C2330: 28003374	GTBX	AFUc15919	1.1E-170	
24362 ENU08157 ANI61C2332: 43784578	GTBX	AFUc10180	2.8E-34	
24363 ENU08158 ANI61C3062: 25081335	GTBX	Y13134	5.7e-120	
24364 ENU08159 ANI61C1605: 6431020	GTBX	AFUc10143	5.5E-28	
24365 ENU08160 ANI61C3064: 221668	GTBX	AFUc13128	8.1E-56	
24366 ENU08161 ANI61C1606: 1693539	GTBX	"AFUc16378, AFUc21308"	"1.1e-30, 9.5e-19"	
24367 ENU08162 ANI61C1607: 52431	GTBX	AFUc06472	6.4E-37	
24368 ENU08163 ANI61C2338: 1791877	GTBX	"AFUc07657, AFUc20776, FGR-03047"	"9.3e-58, 8.4e-27, 7.66-15"	
24369 ENU08164 ANI61C1040 0:1011199	GTBX	"AFUc15768, CALc05180"	"1.7e-65, 3.5e-30"	
24370 ENU08165 ANI61C1040 4:1681456	GTBX	AFUc11156	1.7E-68	
24371 ENU08166 ANI61S2170: 458150	GTBX	AFUc21244	5.8E-49	
24372 ENU08167 ANI61C2340: 11021321	GTBX	AFUc08035	2.2E-21	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24373 ENU08168 ANI61C3071:	Selection Basis GTBX	Database Hit ncbi gi AFUc06001		% id cvrg Description
24374 ENU08169 ANI61C3071: 26562201	GTBX	AFUc11320	9.2E-37	
24375 ENU08170 ANI61C2342: 21100	GTBX	AFUc15644	3E-54	
24376 ENU08171 ANI61C2343: 385998	GTBX	AFUc14858	1.2E-21	
24377 ENU08172 ANI61C1614: 164169	GTBX	"AFUc15021, FGRc09385"	"7.2e-79, 6.5e-61"	
24378 ENU08173 ANI61C2344: 7721143	GTBX	AFUc15170	2.4E-32	
24379 ENU08174 ANIGICI616: 635183	GTBX	AFUc13750	1.9E-41	
24380 ENU08175 ANI61C1618: 784110	GTBX	AFUc10659	3.1E-61	
24381 ENU08176 ANI61C1619: 23851431	GTBX	"AFUc05005, AFUc10889, AFUc21670"	"2.2e-16, 2.4e-24, 2.0e-20"	
24382 ENU08177 ANI61C1041 2:19211718	GTBX	AFUc15311	2.9E-43	
24383 ENU08178 ANI61C1114 1:70041	GTBX	AFUc09651	4.4E-31	
24384 ENU08179 ANI61C1041 5:17132470	GTBX	"AFUc08021, AFUc08021"	"1.5e-89, 2.0e-57"	
24385 ENU08180 ANI61C1041 6:44826	GTBX	AFUc09679	3.7E-37	
24386 ENU08181 ANI61C1114 5:42591	GTBX	CALc04731	4.5E-30	

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aat Blast Blast % ncbi gi Score Score Prob % id cvrg Description 1.8E-72	2.9E-38	"2.2e-50, 1.7e-18"	"3.0e-42, 2.4e-44"	9.8E-26	2.2E-25	8.6E-36	4E-80	2.2E-33	1.3E-47	5.6E-53	7.4E-47	3.5E-57	"2.0e-70, 3.3e-35"
Database Hit AFUc16242	AFUc05157	"AFUc14050, AFUc20977"	"AFUc21878, FGRc17423"	AFUc17331	AFUc12693	AFUc09749	AFUc13580	AFUc03062	AFUc07151	AFUc10559	AFUc02537	AFUc15814	"AFUc15533, AFUc15533"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 24387 ENU08182 ANI61C1114 7:1861347	24388 ENU08183 ANI61C3082: 4961046	24389 ENU08184 ANI61C3085: 184915	24390 ENU08185 ANI61C3086: 61600	24391 ENU08186 ANI61C1042 0:32363461	24392 ENU08187 ANI61C1630: 739967	24393 ENU08188 ANI61C3090: 42814003	24394 ENU08189 ANI61C1632: 3.711	24395 ENU08190 ANI61C1633: 895350	24396 ENU08191 ANI61C3094: 77861	24397 ENU08192 ANI61C1637: 500782	24398 ENU08193 ANI61C2367: 22701947	24399 ENU08194 ANI61C2368: 1548.425	24400 ENU08195 ANI61C3097: 135716

Blast % Prob % id cvrg Description 2.3E-61	"2.4e-38, 5.3e-50"	"9.8e-32, 5.5e-37"	1.7e-84	8.1E-110	"9.9e-11, 4.5e-69"	5.8E-91	2.4E-117	4.3E-26	2.3E-35	"3.0e-40, 4.1e-64, 1.3e-71, 2.4e-61"	"2.6e-29, 1.2e-69"	5.9E-21	1.1E-73
aat Blast Score Score													
Database Hit ncbi gi AFUc14374	"AFUc04312, AFUc04312"	"AFUc09009, FGRc21606"	Y13134	AFUc10437	"AFUc05778, Y13139"	AFUc14823	AFUc10283	AFUc15899	AFUc10300	"AFUc08784, AFUc20323, CALc05827, Y13136"	"AFUc17428, AFUc22468"	FGRc03277	CALc05018
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 24401 ENU08196 ANI61C2369: 33964360	24402 ENU08197 ANI61C1043 0:732430	24403 ENU08198 ANI61C1043 2:1380543	24404 ENU08199 ANI61C1116 3:6151731	24405 ENU08200 ANI61C1116 7:13891628	24406 ENU08201 ANI61C1116 8:6371234	24407 ENU08202 ANI61C1646: 16771930	24408 ENU08203 ANI61C2376: 6071538	24409 ENU08204 ANI61C1648: 1309924	24410 ENU08205 ANIGIC1117 2:3540	24411 ENU08206 ANI61C1044 6:39626140	24412 ENU08207 ANIGIC1117 7:381146	24413 ENU08208 ANI61C1117 8:26.420	24414 ENU08209 ANIGIC1654: 96333

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Seq num Seq id Contig source 24415 ENU08210 ANI61C2383: 772341	Contig source ANI61C2383: 772341	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc13458, AFUc13458"	aat Blast Score Score	Blast Prob "1.4e-69, 6.6e-46"	% id cvrg Description	cription
24416 ENU08211 ANI61C2386: 14731077	ANI61C2386: 14731077			GTBX	AFUc05516		2.4E-35		
24417 ENU08212 ANI61C1657: 36.718	ANI61C1657: 36718			GTBX	AFUc01220		3.3E-30		
24418 ENU08213 ANI61C2387: 419792	ANI61C2387: 419792			GTBX	"AFUc08391, U00093"		"1.1e-29, 1.5e-28"		
24419 ENU08214 ANI61C1045 2:27363671	ANI61C1045 2:27363671			GTBX	"AFUc01446, AFUc03449"		"3.6e-49, 5.3e-62"		
24420 ENU08215 ANI61C1045 5:102916040	ANI61C1045 5:102916040			GTBX	"AFUc02402, AFUc13896, AFUc15794, FGRc10936, FGRc19244"		"7.6e-13, 4.1e-90, 9.2e-59, 4.8e-08, 2.7e-24"		
24421 ENU08216 ANI61C1118 4:29301174	ANI61C1118 4:29301174			GTBX	"AFUc12122, AFUc19794"		"8.4e-30, 3.5e-11"		
24422 ENU08217 ANI61C1118 5:724365	ANI61C1118 5:724365			GTBX	AFUc17013		5.9E-43		
24423 ENU08218 ANI61C1118 6:66526341	ANI61C1118 6:66526341			GTBX	AFUc15274		7.9E-30		
24424 ENU08219 ANI61C1118 7:52556412	ANI61C1118 7:52556412			GTBX	AFUc11057		2.3E-165		
24425 ENU08220 ANI61C1118 8:37861817	ANI61C1118 8:37861817			GTBX	"AFUc03500, FGRc12085"		"3.9e-11, 1.6e-27"		
24426 ENU08221 ANI6IC1118 9:437772	ANI61C1118 9:437772			GTBX	AFUc05827		2.1E-56		
24427 ENU08222 ANI61C2396: 41053424	ANI61C2396: 41053424			GTBX	AFUc20773		1.9E-45		

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Seq num Seq id 24428 ENU08223	Contig source ANI61C1667: 4582025	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc01694, AFUc03534, AFUc09885"	aat Blast Score Score	Blast Prob % "5.0e-13, 3.7e-37, 1.5e-68"	% id cvrg De	Description
24429 ENU08224 ANI61C1 0:25273	ANI61C1046 0:25273230			GTBX	"AFUc10414, FGRc04734"		"3.0e-47, 4.3e-09"		
24430 ENU08225 ANI61C1 1:77679	ANI61C1119 1:77679			GTBX	AFUc15108		3.8E-31		
24431 ENU08226 ANI61C1 5:24674	ANI61C1046 5:24674478			GTBX	"AFUc12339, AFUc12339"		"2.1e-67, 2.9e-31"		
24432 ENU08227 ANI61C1 8:49975	ANI61C1046 8:49975533			GTBX	AFUc08587		8.5E-68		
24433 ENU08228	ANI61C1119 9:60490			GTBX	AFUc14731		1.9E-24		
24434 ENU08229	ANI61C1672: 893597			GTBX	AFUc14113		6.4E-90		
24435 ENU08230 ANI61C500:2 84899	ANI61C500:2 84899			GTBX	AFUc12648		1.6E-30		
24436 ENU08231 ANI61C5 201087	ANI61C504:7 201087			GTBX	FGRc12152		1.8E-64		
24437 ENU08232 ANI61C5 2823902	ANI61C508:3 2823902			GTBX	AFUc04843		3.5E-38		
24438 ENU08233 ANI61C1 7:17618	ANI61C1047 7:1761819			GTBX	"FGRc06621, FGRc19870, FGRc21283"		"2.5e-17, 1.7e-14, 8.5e-50"		
24439 ENU08234 ANI61C1 6111742	ANI61C1683: 6111742			GTBX	"AFUC01385, AFUC06858, CALC02967"		"5.7e-25, 1.9e-46, 7.0e-43"		
24440 ENU08235 ANI61C513:4 15729	ANI61C513:4 15729			GTBX	FGRc09331		4.8E-67		
24441 ENU08236 ANI61CJ 414704	ANI61C1690: 414704			GTBX	AFUc04365		1.2E-36		

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24442 ENU08237 ANI61C524:1 24354 24443 ENU08238 ANI61C525:7 223233	Selection Basis GTBX GTBX	Database Hit ncbi gi AFUc15671 "AFUc09623, AFUc15525,	aat Blast Blast Score Score Prob 8.4E-83 "1.0e- 131,	% id cvrg Description
24444 ENU08239 ANI61C1049 0:56436771	GTBX	FGRc16821, Z12576, Y13138" "AFUc05896, CALc06013"	8.9e- 312, 4.1e-18, 0.0, 6.5e-82" "4.7e-64, 3.9e- 188"	
24445 ENU08240 ANI61C528:4 8314175 24446 ENU08241 ANI61C528:7 4498035	GTBX	AFUc13014 AFUc10735	1.1E-65 1.8E-63	
24447 ENU08242 ANI61C1049 2:10472721	GTBX	"AFUc09485, AFUc15798"	"4.7e-32, 1.0e-98"	
24448 ENU08243 ANI61C1049 2:38424935	GTBX	"AFUc04378, AFUc07681"	"9.3e-63, 1.7e-11"	
24449 ENU08244 ANI61C529:4 2431	GTBX	AFUc11443	2.3E-52	
24450 ENU08245 ANI61C1049 5:37176173	GTBX	"AFUc05971, AFUc11732, CALc05629, CALc05629"	"6.4e-92, 9.2e- 131, 1.3e- 193, 6.0e-37"	
24451 ENU08246 ANI61C534:4 5335332	GTBX	AFUc08068	3.2E-56	
24452 ENU08247 ANI61C534:7 7396453	GTBX	"AFUc19364, FGRc04608, FGRc14414"	"3.5e-33, 1.7e-10, 3.2e-25"	

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aat Blast Blast % Score Score Prob % id cvrg Description 1.2E-32	"4.4e- 109, 3.4e-42, 4.8e-08"	1.1e-30, 5.7e- 131,	2.6e- 137, 2.1e-79, 2.2-11"	2E-70	2.2E-61	6.9E-26	4.7E-45	6.9E-42	8.2E-34	"2.0e-55, 1.5e-25, 1.6e-29"	2.2E-38	"1.8e-26, 1.6e-23"
Selection Basis Database Hit ncbi gi Sco GTBX AFUc09242	GTBX "AFUc15779, FGRc15231, X59720"	GTBX "AFUc10780, CALc05902, Z71257"	GTBX "AFUc15540, FGRc10976, FGRc25479"	GTBX AFUc11194	GTBX CALc04732	GTBX AFUc13681	GTBX AFUc00564	GTBX AFUc08057	GTBX AFUc05897	GTBX "AFUc11352, FGRc00210,	GTBX AFUC12416	GTBX "AFUc05079, AFUc05496"
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24453 ENU08248 ANIG1C536:7 47385	24454 ENU08249 ANI61C540:1 115107	24455 ENU08250 ANI61C543:5 41726	24456 ENU08251 ANI61C8110: 25905977	24457 ENU08252 ANI61C8111: 1800544	24458 ENU08253 ANI61C8113: 12232311	24459 ENU08254 ANI61C8115: 27483329	24460 ENU08255 ANI61C8118: 25442122	24461 ENU08256 ANI61C556:1 4522621	24462 ENU08257 ANI61C556:3 6093139	24463 ENU08258 ANI61C8121: 828109	24464 ENU08259 ANI61C8123: 25791657	24465 ENU08260 ANI61C8127: 11502

# cica e e e e e e e e e e

aat Blast Blast % Score Score Prob % id cvrg Description 1.0e-107	"2.3e-30, 5.9e-31"	"8.6e-47, 1.0e-69"	2.2E-98	3.1E-35	5.9E-43	3.3E-35	4.3E-59	1.6e-32	4.1E-88	2.4E-23	4.6e-19	5.1E-25	4.4E-69
Database Hit ncbi gi	"AFUc06900, AFUc14568"	"AFUc04078, CALc05482"	AFUc13396	FGRc04774	AFUc09285	AFUc14097	AFUc11487	Y13138	AFUc15484	AFUc01706	Y13139	AFUc12228	AFUc10307
Primer Selection 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq Primer num Seq id Contig source 5 pos 24466 ENU08261 ANI61C565:3 4745173	24467 ENU08262 ANI61C7402: 1111536	24468 ENU08263 ANI61C7406: 1092374	24469 ENU08264 ANI61C8136: 37744745	24470 ENU08265 ANI61C8139: 43064841	24471 ENU08266 ANI61C576:4 5590	24472 ENU08267 ANI61C8142: 20333024	24473 ENU08268 ANI61C7414: 299789	24474 ENU08269 ANI61C8146: 34023	24475 ENU08270 ANI61C8149: 123658	24476 ENU08271 ANI61C8154: 61113	24477 ENU08272 ANI61C7427: 71274	24478 ENU08273 ANI61C8158: 26341709	24479 ENU08274 ANI61C591:6 5921

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Seq num Seq id 24480 ENU08275	Contig source ANI61C6703: 32064413	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc15895, FGRc12402"	aat Blast Score Score	Blast Prob "3.6e-40, 6.1e-31"	% id cvrg Description	Description
24481 ENU08276 ANI61C6705: 48445990	ANI61C6705: 48445990			GTBX	"AFUc13044, AFUc15912"		"2.2e- 106, 3.6e-90"		
24482 ENU08277 ANI61C6710: 12201609	ANI61C6710: 12201609			GTBX	AFUc01691		1.9E-27		
24483 ENU08278 ANI61C8171: 3471607	ANI61C8171: 3471607			GTBX	"AFUc08832, AFUc09980, FGRc01231"		"4.7e-50, 9.0e-34, 4.2e-51"		
24484 ENU08279 ANI61C8173: 4402176	ANI61C8173: 4402176			GTBX	"AFUc05587, AFUc07211, AFUc08234, AFUc21621"		"1.4e- 107, 1.1e-65, 4.8e-95,		
24485 ENU08280 ANI61C6719: 484128	ANT61C6719: 484128			GTBX	AFUc15031		1.6E-36		
24486 ENU08281 ANI61C6720: 349919	ANI61C6720: 349919			GTBX	AFUc13243		2.8E-68		
24487 ENU08282 ANI61C7451: 17512032	ANI61C7451: 17512032			GTBX	AFUc01939		1.1E-51		
24488 ENU08283 ANI61C8185: 4311227	ANI61C8185: 4311227			GTBX	"AFUc00988, CALc06038"		"3.3e-60, 2.8e-38"		
24489 ENU08284 ANI61C7457: 434208	ANI61C7457: 434208			GTBX	AFUc15970		4.2E-78		
24490 ENU08285 ANI61C 612949	ANI61C6728: 612949			GTBX	AFUc08768		1.8E-44		
24491 ENU08286 ANI61C8188: 32011912	ANI61C8188: 32011912			GTBX	"AFUc01114, AFUc18282, AFIC20635"		"1.3e-35, 1.4e-22, 8.8e-10"		
24492 ENU08287 ANI61C7459: 69741	ANI61C7459: 69741			GTBX	AFUc04086		4E-82		

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Seq num Seq id 24493 ENU08288	Contig source ANI61C6730: 156509	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc03916	aat Blast Score Score	Blast Prob % 1.4E-26	% % id cvrg Description
24494 ENU08289 ANI61C8191: 1018156	ANI61C8191: 1018156			GTBX	AFUc09445		3.2E-100	
24495 ENU08290 ANI61C6734: 56076701	ANI61C6734: 56076701			GTBX	"AFUc21317, Z71257"		"6.1e-07, 1.4e-32"	
24496 ENU08291 ANI61C7465: 19542550	ANI61C7465: 19542550			GTBX	AFUc14734		3E-161	
24497 ENU08292 ANI61C8194: 20762470	ANI61C8194: 20762470			GTBX	Y13137		8.2e-186	
24498 ENU08293 ANI61C6738: 54894467	ANI61C6738: 54894467			GTBX	"AFUc01683, CALc04817, FGR-00806"		"1.6e-45, 3.1e-21,	
24499 ENU08294 ANI61C7475: 1427483	ANI61C7475: 1427483			GTBX	"AFUc17643, FGRc05979"		"1.2e-08, 1.2e-45"	
24500 ENU08295 ANI61C7476: 281165	ANI61C7476: 281165			GTBX	"AFUc02079, AFUc09659"		"3.0e-52, 7.5e-07"	
24501 ENU08296 ANI61C7479: 864121	ANI61C7479: 864121			GTBX	AFUc04883		1.9E-88	
24502 ENU08297 ANI61C6750: 1592800	ANI61C6750: 1592800			GTBX	AFUc02986		4.9E-36	
24503 ENU08298 ANI61C7483: 51606015	ANI61C7483: 51606015			GTBX	"AFUc12789, Y13134"		"3.0e-68, 1.5e-12"	
24504 ENU08299 ANI61C7486: 1350379	ANI61C7486: 1350379			GTBX	"AFUc02949, AFUc04582, FGRc10932"		"7.7e-71, 5.6e-39, 2.7e-18"	
24505 ENU08300 ANI61C6759: 26491266	ANI61C6759: 26491266			GTBX	"AFUc10464, CALc06073"		"2.9e-71, 4.8e-98"	
24506 ENU08301 ANI61C7491: 4811258	ANI61C7491: 4811258			GTBX	AFUc15766		3.3E-67	

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24507 ENU08302 ANI61C6763: 8451658	Selection Basis GTBX	Database Hit ncbi gi "AFUc13390, AFUc13390"	aat Blast Blast Score Score Prob "2.5e-45,	% % id cvrg Description 45,
24508 ENU08303 ANI61C7493: 185441	GTBX	AFUc15810	1.4E-236	.36
24509 ENU08304 ANI61C7499: 18932258	GTBX	AFUc09120	5.7E-46	9
24510 ENU08305 ANI61C6771: 95577	GTBX	"FGRc02670, Y13139"	"4.1e-40, 8.9e-18"	40, 8"
24511 ENU08306 ANI61C6780: 15421913	GTBX	"AFUc17233, FGRc05382"	"7.2e-52, 1.2e-14"	52, 4"
24512 ENU08307 ANI61C6782: 1381073	GTBX	AFUc12300	9.2E-80	0;
24513 ENU08308 ANI61C6786: 269868	GTBX	"AFUc03905, CALc03405"	"6.3e-25, 3.1e-20"	25, 0"
24514 ENU08309 ANI61C6789: 1667164	GTBX	AFUc12649	3E-156	9
24515 ENU08310 ANI61S448:4 50153	GTBX	FGRc24169	2.3E-21	11
24516 ENU08311 ANI61C6792: 7001644	GTBX	"AFUc06967, FGRc12581"	"7.2e-93 <sub>,</sub> 6.8e-27"	93, 7"
24517 ENU08312 ANI61C6797: 103550	GTBX	Y13135	1.3e-48	8
24518 ENU08313 ANI61S2206: 32628	GTBX	AFUc12261	2E-33	
24519 ENU08314 ANI61C3111: 393719	GTBX	AFUc15581	2.3E-67	25
24520 ENU08315 ANI61C3114: 2476	GTBX	AFUc10952	1E-22	

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aat Blast Blast % Score Score Prob % id cvrg Description 8.4E-42	"2.9e.45, 3.3e.72"	6.5e-14	"7.3e-07, 5.1e-25"	1.4E-33	2E-71	1.3E-32	6.5E-33	1.6e-24	6.5E-33	3.3E-46	"1.6e-65, 6.8e-08"	"1.9e-38, 1.1e-41, 1.9e-46"	"9.6e-59, 1.2e-88"
tion s Database Hit ncbi gi X AFUc14123	X "AFUc15397, AFUc15397"	X AI001370	X "AFUc10109, FGRc24183"	X AFUc09498	X AFUc10750	X AFUc21643	X AFUc06894	X Z71256	X AFUc12485	X AFUc01209	X "AFUc06238, AFUc21228"	IX "AFUc03672, CALc04359, V13139"	- ,
Primer Primer Selection 5 pos 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GТВХ	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq num Seq id Contig source : 24521 ENU08316 ANI61C3120: 317649	24522 ENU08317 ANI61C3122: 3329	24523 ENU08318 ANI61C3133: 7761003	24524 ENU08319 ANI61C2406: 34768	24525 ENU08320 ANI61C3138: 18002489	24526 ENU08321 ANI61C2409: 23820	24527 ENU08322 ANI61C1120 5:8421238	24528 ENU08323 ANI61C1120 5:77737272	24529 ENU08324 ANI61C1120 5:100411038	24530 ENU08325 ANI61C1120 5:110461135	24531 ENU08326 ANI61S1516: 546243	24532 ENU08327 ANI61C2411: 175744	24533 ENU08328 ANI61C2411: 23611216	24534 ENU08329 ANI61C3145: 40772208

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aat Blast Blast % iit ncbi gi Score Score Prob % id cvrg Description 8	3.6E-46	59, "1.3e-83, "0, 6.3e-32, "3.2, 6.3e-32, 6.3e-3		4 3.7E-24	0 6.5E-27	6 6.7E-28	49, "5.5e-44, 6, 1.6e-28,			5 1.2E-47	8 2.8E-47	55, "2.0e-63, 5.7e-
Database Hit CALc04288	AFUc14655	"AFUc105869, AFUc10580, CAL-05396"	AFUc15114	AFUc16004	AFUc03940	AFUc14756	"AFUc03549, AFUc13726,	AFUC13/20 "AFUC11188, U00093"	AFUc21873	AFUc07435	CALc05628	"AFUc11755, Y13135"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos												
Seq num Seq id Contig source 24535 ENU08330 ANI61C3148: 2301073	24536 ENU08331 ANI6IC1121 0:954656	24537 ENU08332 ANI61C1121 1:1639690	24538 ENU08333 ANI61C1121 4:784401	24539 ENU08334 ANI61C1121 5:541134	24540 ENU08335 ANI61C2420: 22262459	24541 ENU08336 ANI61C2421: 10571414	24542 ENU08337 ANI61C2422: 2571093	24543 ENU08338 ANI61C3152: 4393434	24544 ENU08339 ANI61C3157: 40.494	24545 ENU08340 ANI61C3158: 35822955	24546 ENU08341 ANI61C1122 3:26142006	24547 ENU08342 ANI61C1122 9:51796489

# ofton of the subure

aat Blast Blast % ncbi gi Score Score Prob % id cvrg Description , 4.3e-28, 4.5e-32"	i, "2.1e-19, 9.6e-50"	4.8E-24	2.1E-53	), "1.2e-28, 2.5e-53, 1.1e-51"		0.0	3.1E-47	3.9E-26	1.IE-73	4.3E-26	5, "4.9e-32, " 9.8e-62"	6.3E-206	2.2E-37
Database Hit "AFUc01570, AFUc08276"	"AFUc00996, Y13134"	CALc05020	AFUc13944	"AFUc01000, AFUc04109, FGRc04331"	"AFUc14997, AFUc14997"	Y13138	CALc06073	AFUc13411	AFUc14288	AFUc03044	"AFUc12955" AFUc12955"	AFUc14427	AFUc08082
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 5 24548 ENU08343 ANI61C2431: 97659	24549 ENU08344 ANI61C1705: 49956299	24550 ENU08345 ANI61C3165: 211726	24551 ENU08346 ANI61C3166: 752138	24552 ENU08347 ANI61C2437: 22003538	24553 ENU08348 ANI61C1123 0:32141952	24554 ENU08349 ANI61C1050 1:62637127	24555 ENU08350 ANI61C1050 6:2538	24556 ENU08351 ANI61C1050 8:52279	24557 ENU08352 ANI61C3170: 1199657	24558 ENU08353 ANI61C1713: 26451891	24559 ENU08354 ANI61C2446: 84449	24560 ENU08355 ANI61C3177: 31536	24561 ENU08356 ANIGIC2449: 872402

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Seq num Seq id Contig source 24576 ENU08371 ANI61C2461: 2065212 24577 ENU08372 ANI61C2465: 6983702	Contig source ANI61C2461: 2065212 ANI61C2465: 6983702	Primer 5 pos	Primer 3 pos	Selection Basis GTBX GTBX	Database Hit ncbi gi AFUc10369 "AFUc07667, AFUc12566, AFUc13531,	aat Blast Blast Score Score Prob 8.3E- "4.3e- 3.3e-?	Blast % Prob % id cvrg Description 8.3E-53 "4.3e-12, 1.1e-38, 3.3e-23,
ENU08373	24578 ENU08373 ANI61C3199: 15902454	·		GTBX	AFUC14327, AFUC14338, AFUC15132, FGRC00835, FGRC17112" "AFUC05935, AFUC15519"	2.0 2.5 2.5 6.0 6.0 1.2 1.3	2.0e-42, 2.0e-63, 2.5e-52, 6.0e-27, 1.2e-08" "1.3e-10,
ENU08374	24579 ENU08374 ANI61C1126 0:326605 24580 ENU08375 ANI61C1126 3:30527			GTBX	"AFUc15094, AFUc15094, Y13134" AFUc09950	.12. 4.6 3.4 3.4	"2.3e-14, 4.6e-17, 2.0e-24" 3.4E-34
ENU08376	24581 ENU08376 ANI61C1053 4:344592 24582 ENU08377 ANI61C1053 5:45433779			GTBX	AFUc13512 AFUc14535	2.2	2.2E-56 1.7E-97
ENU08378	24583 ENU08378 ANIGIC1126 4:35051 24584 ENU08379 ANIGIC1126 8:188526			GTBX	AFUc09251 AFUc09884	2.3	2.3E-41 2.5E-21
ENU08380	24585 ENU08380 ANI61C1743: 4121446			GTBX	"AFUc07667, AFUc08168, AFUc08900, AFUc14327"		"3.8e-15, 7.4e-50, 4.1e-11, 5.1e-48"
ENU08381	24586 ENU08381 ANI61C2475: 1147548			GTBX	AFUc02096	1.4	1.4E-43 1.2E.22
' ENU08382	24587 ENU08382 ANI61C2479: 12981026			GTBX	AFUc06657	1.7	E-22

c												
% cvrg Description												
% d cvrg I												
% id 54, 5,	4	22, 0,	· 으		20	25	68,	33, 5"	·	.57, 19"	36,	63,
Blast Prob "2.7e-54, 6.8e-95, 3.0e-	4.5E-34	"7.0e-22, 1.4e-10, 7.8e-21"	2.4E-40	1E-39	6.8E-50	1.4E-62	"9.7e-68, 3.5e-10"	"3.0e-33, 1.2e-16, 7.2e-15"	0:0	"3.1e-57, 1.3e-19"	"5.6e-36, 1.0e-18,	"1.6e-63 8.0e-19"
Blast												
aat Score												
ncbi gi												
	10	512, 83, 35"	52	81	49	94	939, 25"	284, 195,	5	219, 227"	407, .67,	763, 182"
Database Hit "AFUc04995, AFUc12046, Y13140"	AFUc15910	"AFUc03512, AFUc08783, EGR 19235"	AFUc15452	AFUc05281	AFUc16564	AFUc09694	"AFUc11939, FGRc23525"	"AFUc01284, AFUc02695, AFITC04437"	U00094	"AFUc03219, AFUc12227"	"AFUc09407, FGRc11267, EGP : 11267"	"AFUc21763, FGRc25482"
u o												, - , ,
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos												
Primer 5 pos												
	C1054 741	C1127 548	21127 2773	\$1589:	22482: 0	C1757: 857	21758: 099	C1128 2349	C1055 5219	C1055 2414	C1761:	C2491:
Contig source ANI61C1054 1:2168395	24589 ENU08384 ANI61C1054 5:959741	24590 ENU08385 ANI61C1127 7:180648	24591 ENU08386 ANI61C1127 8:30842773	24592 ENU08387 ANI61S1589: 24506	24593 ENU08388 ANI61C2482: 122700	24594 ENU08389 ANI61C1757: 24002857	24595 ENU08390 ANI61C1758: 66145099	24596 ENU08391 ANI61C1128 0:7362349	24597 ENU08392 ANI61C1055 5:46885219	24598 ENU08393 ANI61C1055 9:15722414	24599 ENU08394 ANI61C1761: 22813753	24600 ENU08395 ANI61C2491: 1150365
3383	108384	108385	108386	108387	108388	108389	108390	108391	108392	108393	J08394	108395
∞	9 ENU	0 ENU	I ENU	2 ENU	3 ENU	4 ENU	S ENU	6 ENU	7 ENC	8 ENC	99 ENL	O ENL
Seq num 24588	2458	2459	2459	2459	2459	2459	2459	2459	2459	2459	2459	246(

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Seq num Seq id 24601 ENU08396	Contig source ANI61C1765: 38494804	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc08160	aat Blast Score Score	Blast Prob % id 2.4E-108	% % id cvrg Description
24602 ENU08397 ANI61C1768: 1071245	AM61C1768: 1071245			GTBX	"CALc05020, FGRc07538, Y13134"		"2.8e- 1133, 2.6e- 1107, 2.6e-	
24603 ENU08398 ANI61C1769: 630424	ANI61C1769: 630424			GTBX	AFUc15659		1.1E-24	
24604 ENU08399 ANI61C1056 0:379587	ANI61C1056 0:379587			GTBX	FGRc10510		1.5E-36	
24605 ENU08400 ANI61C1129 1:6803	ANI61C1129 1:6803			GTBX	"AFUc01382, AFUc06747"		"2.4e-16, 2.3e- 108"	
24606 ENU08401 ANI61C1129 2:9921827	ANI61C1129 2:9921827			GTBX	"AFUc01815, AFUc19145"		"4.1e-10, 5.5e-40"	
24607 ENU08402 ANI61C1129 3:1130708	ANI61C1129 3:1130708			GTBX	"AFUc09000, Y13134"		"3.5e-81, 4.3e-40"	
24608 ENU08403 ANI61C112' 4:28565 ·	ANI61C1129 4:28565			GTBX	AFUc04474		6E-68	
24609 ENU08404 ANI61C1129 8:975145	ANI61C1129 8:975145			GTBX	"CALc04432, FGRc05226"		"8.9e-80, 2.7e-19"	
24610 ENU08405 ANI61C1129 9:13501568	ANI61C1129 9:13501568			GTBX	CALc03902		7E-40	
24611 ENU08406 ANI61C1774: 450851	ANI61C1774: 450851			GTBX	AFUc11966		5.9E-46	
24612 ENU08407 ANI61C1779: 391849	ANI61C1779: 391849			GTBX	AFUc12781		9.6E-30	
24613 ENU08408 ANI61C1057 4:957691	ANI61C1057 4:957691			GTBX	AFUc09666		2.4E-38	

# ceco ceco

Seq num Seq id 24614 ENU08409	Seq id Contig source ENU08409 ANI61C1781: 5532	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc09001, CALc06053"	aat Blast Score Score	Blast % Prob % id cvrg Description "3.6e-17, 7.5e-30"	
24615 ENU08410 ANI61C614:8 1879	ANI61C614:8 1879			GTBX	AFUc21798		8.5E-31	
24616 ENU08411 ANI61C617:7 90344	ANI61C617:7 90344			GTBX	AFUc01603		8.4E-73	
24617 ENU08412 ANI61C1058 7:1251577	ANI61C1058 7:1251577			GTBX	"AFUc13537, AFUc15937, AFUc16854, AFIC18057"		"6.1e-43, 9.1e-33, 5.3e-07, 7.5e-60"	
24618 ENU08413 ANI61C1058 9:47176120	ANI61C1058 9:47176120			GTBX	AFUc16933		8.6E-28	
24619 ENU08414 ANI61C621:9 8827	ANI61C621:9 8827			GTBX	AFUc13969		3.8E-62	
24620 ENU08415 ANI61C629:1 4261674	ANI61C629:1 4261674			GTBX	AFUc10182		2.2E-44	
24621 ENU08416 ANI61C632:2 6152967	ANI61C632:2 615.2967			GTBX	AFUc13337		2.6E-69	
24622 ENU08417 ANI61C638:1 513642	ANI61C638:1 513642			GTBX	AFUc13559		1.7E-119	
24623 ENU08418 ANI61C8202: 23272693	ANI61C8202: 23272693			GTBX	AFUc09447		1.7E-72	
24624 ENU08419 ANI61C8205: 1564	ANI61C8205: 1564			GTBX	AFUc11001		1.7E-28	
24625 ENU08420 ANI61C8211: 438914	ANI61C8211: 438914			GTBX	AFUc10534		3.7E-117	
24626 ENU08421 ANI61C8212: 14801118	ANI61C8212: 1480.1118			GTBX	AFUc15391		3.5E-112	
24627 ENU08422 ANI61C8220: 4444	ANI61C8220: 4444			GTBX	AFUc05936		2.8E-55	

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Seq num Seq id 24628 ENU08423	Contig source ANI61C8225: 1437173	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc05414, CALc04219"	aat Blast Score Score	Blast Prob % "7.7e-59, 4.0e-44"	% id cvrg Description	
24629 ENU08424 ANI61C661:3 918	ANI61C661:3 918			GTBX	AFUc07993		4.6E-33		
24630 ENU08425 ANI61C7502: 20854478	ANI61C7502: 20854478			GTBX	"AFUc11007, Y13135"		"2.0e-65, 1.3e- 154"		
24631 ENU08426 ANI61C7503: 20462255	ANI61C7503: 20462255			GTBX	Y13134		3.1e-237		
24632 ENU08427 ANI61C823 608326	ANI61C8233: 608326			GTBX	"AFUc15337, AFUc15337"		"3.3e- 113, 4.3e-		
24633 ENU08428 ANI61C823 14732074	ANI61C8235: 14732074			GTBX	"AFUc12073, CALc06007"		"3.1e-32, 1.9e-83"		
24634 ENU08429 ANI61C8236: 5421400	ANI61C8236: 5421400			GTBX	AFUc00714		6.8E-52		
24635 ENU08430 ANI61C823 9501813	ANI61C8238: 9501813			GTBX	AFUc20930		2.6E-32		
24636 ENU08431 ANI61C670:3 64585	ANI61C670:3 64585			GTBX	AFUc13626	٠	6.8E-35		
24637 ENU08432 ANI61C671:1 12549	ANI61C671:1 12549			GTBX	"AFUc15558, AFUc15558"		"2.0e-65, 4.8e-61"		
24638 ENU08433 ANI61C678:8 1430	ANI61C678:8 1430			GTBX	AFUc13964		1.5E-29		
24639 ENU08434 ANI61C8245: 1570437	ANI61C8245: 1570437			GTBX	"AFUc14341, FGRc04315"		"1.6e- 105, 5.4e-36"		
24640 ENU08435 ANI61C682:2 2131222	ANI61C682:2 2131222	- >		GTBX	AFUc15961		1.5E-25		

Sed		Primer	Primer	Selection		aat Blast Blast	%
num Seq id Contig source 24641 ENU08436 ANI61C686:5 3476396	Contig source ANI61C686:5 3476396	5 pos	3 pos	Basis GTBX	Database Hit ncbi gi "AFUc10299, AFUc13858, AFUc17463"	ore Score Prob "5.8e-31, 4.5e-20, 1.1e-57"	% id cvrg Description
24642 ENU08437 ANI61C686:7 5986771	ANI61C686:7 5986771			GTBX	AFUc04010	1.6E-37	
24643 ENU08438 ANI61C8251: 422483	ANI61C8251: 422483			GTBX	"AFUc09565, AFUc20070"	"1.2e- 104, 1 6e-30"	
24644 ENU08439 ANI61C7527: 16715042	) ANI61C7527: 16715042			GTBX	"AFUc10374, AFUc13490, AFUc18055"	"9.3e- 166, 7.1e- 130, 2.1e-26"	
24645 ENU08440 ANI61C8257: 51896135	ANI61C8257: 51896135			GTBX	"AFUc03480, AFUc13151"	"4.8e-40, 6.3e-85"	
24646 ENU08441 ANI61C699:7 57494	ANI61C699:7 57494			GTBX	FGRc01809	2.4E-42	
24647 ENU08442 ANI61C6 6162355	2 ANI61C6802: 6162355			GTBX	"AFUc00490, FGRc08907, FGRc25065"	"4.3e-13, 1.1e-44, 1.9e-32"	
24648 ENU08443 ANI61C6 300656	300656			GTBX	AFUc10335	5.4E-24	
24649 ENU08444 ANI61C6 1450522	H ANI61C6804: 1450522			GTBX	"AFUc02585, AFUc16083, AFUc18105"	"2.3e-28, 5.8e-13, 2.4e-10"	
24650 ENU08445 ANI61C6 531136	5 ANI61C6805: 531136			GTBX	AFUc13932	4.2E-39	
24651 ENU08446 ANI61C7 1513	5 ANI61C7536: 1513			GTBX	AFUc15302	9.7E-24	
24652 ENU08447 ANI61C7 1238224	7 ANI61C7537: 12382244			GTBX	AFUc06075	1.5E-85	
24653 ENU08448 ANI61C6809: 146427	3 ANI61C6809: 146427			GTBX	AFUc11377	2.2E-23	

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aat Blast Blast % Score Score Prob % id cvrg Description 1.1E-34	1.5E-29	"2.1e-45, 7.2e-47"	1.5E-46	"4.8e-38, 8.3e-26"	"8.0e-47, 4.6e-07"	1.7E-82	5.2E-54	"2.7e-28, 8.6e-14"	1.3E-23	1.6E-49	1.6E-21	9.5E-45	"1.2e-17, 3.4e-56"
tion Database Hit ncbi gi K AFUc07452	K AFUc19773	X "AFUc04808, AFUc04808"	X AFUc15466	X "AFUc11101, AFUc11101"	X "AFUc15495, FGRc16134"	X AFUc14280	X FGRc10208	X "AFUc04568, FGRc00446"	X FGRc20509	X AFUc03505	X AFUc15334	X AFUc14069	X "CALc03297, Y13139"
r Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 5 24654 ENU08449 ANI61C8269: 46569	24655 ENU08450 ANI61C6810: 56796098	24656 ENU08451 ANI61C8270: 42731	24657 ENU08452 ANI61C8271: 98634	24658 ENU08453 ANI61C7542: 122989	24659 ENU08454 ANI61C7543: 1033176	24660 ENU08455 ANI61C8272: 11511600	24661 ENU08456 ANI61C6815: 1176454	24662 ENU08457 ANI61C7549: 1848425	24663 ENU08458 ANI61C8279: 1068691	24664 ENU08459 ANI61C6820: 1111501	24665 ENU08460 ANI61C8286: 479137	24666 ENU08461 ANI61C8286: 8391285	24667 ENU08462 ANI61C6829: 1840166

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24668 ENU08463 ANI61C8288:	Selection Basis GTBX	Database Hit ncbi gi AFUc05810	aat Blast Blast % Score Score Prob % id cvrg 2.6E-31	g Description
24669 ENU08464 ANI61C6831: 1481585	GTBX	"AFUc04998, FGRc01824"	"5.7e-56, 3.5e-16"	
24670 ENU08465 ANI61C6834: 357867	GTBX	"AFUc12667, AFUc15842"	"8.8e-56, 2.3e-15"	
24671 ENU08466 ANI61C7563: 1403972	GTBX	AFUc06136	1.6E-52	
24672 ENU08467 ANI61C6835: 6791407	GTBX	AFUc03378	6.6E-21	
24673 ENU08468 ANI61C8295: 3361098	GTBX	"FGRc00692, FGRc11948"	"3.8e-30, 3.3e-22"	
24674 ENU08469 ANI61C7566: 1430741	GTBX	AFUc19723	3.7E-27	
24675 ENU08470 ANI61C6839: 58695612	GTBX	"AFUc04055, AFUc05745"	"3.1e-13, 8.0e-61"	
24676 ENU08471 ANI61C8299: 7163012	GTBX	"AFUc09176, AFUc09176, FGRc09522"	"1.3e- 165, 2.6e-63, 7.0e-09"	
24677 ENU08472 ANI61C7570: 5831210	GTBX	FGRc00007	2.2E-68	
24678 ENU08473 ANI61C7571: 608210	GTBX	AFUc10686	1E-25	
24679 ENU08474 ANI61C7577: 78566	GTBX	AFUc00513	8.2E-23	
24680 ENU08475 ANI61C7578: 25392834	GTBX	AFUc02252	3.3E-31	
24681 ENU08476 ANI61C7587: 23482067	GTBX	FGRc12388	3E-31	

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24682 ENU08477 ANI61C7588:	Selection Basis GTBX	Database Hit ncbi gi "AFUc06763, AFUc07411,	aat Blast 8% Score Score Prob % id cvrg Description "2.5e-71, 1.4e-13,
24683 ENU08478 ANI61S519:2. .592	GTBX	FGRc07962, FGRc16898"	"1.1e-09, 1.8e-29"
24684 ENU08479 ANI61C7591: 10151599	GTBX	AFUc12136	2.1E-78
24685 ENU08480 ANI61C6863: 15731244	GTBX	AFUc10542	7.8E-26
24686 ENU08481 ANI61C6864: 29924626	GTBX	"AFUc07814, CALc01848, Z17256"	"2.5e-77, 6.1e-27, 2.2e-30"
24687 ENU08482 ANI61C6870: 94973	GTBX	"AFUc09260, CALc05985"	"1.4e-91, 4.6e-57"
24688 ENU08483 ANI61C6874: 50930	GTBX	AFUc15201	8.3E-117
24689 ENU08484 ANI61C6875: 4781035	GTBX	"AFUc15186, AFUc15186"	"2.1e-45, 9.8e-52"
24690 ENU08485 ANI61C6883: 6281	GTBX	AFUc08480	2.3E-27
24691 ENU08486 ANI61C6883: 15381254	GTBX	AFUc08221	6.7E-38
24692 ENU08487 ANI61C6888: 24052970	GTBX	AFUc11742	1.8E-66
24693 ENU08488 ANI61C6890: 1004189	GTBX	AFUc08698	4E-54
24694 ENU08489 ANI61C6890: 18982209	GTBX	AFUc09533	2.4E-56
24695 ENU08490 ANI61C6891: 16911221	GTBX	AFUc03109	5.6E-25

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24696 ENU08491 ANI61C6896: 960191	Selection Basis GTBX	Database Hit ncbi gi AFUc14439	aat Blast Blast Score Score Prob 6.5E-64	% id cvrg Description
24697 ENU08492 ANI61C6897: 9776	GTBX	AFUc12120	2E-37	
24698 ENU08493 ANI61S2306: 399.4	GTBX	"AFUc13642, Y13138"	"4.5e-52, 4.1e-09"	
24699 ENU08494 ANI61C3208: 14471953	GTBX	AFUc10936	5.8E-66	
24700 ENU08495 ANI61C3209: 9562284	GTBX	AFUc15271	8.2E-44	
24701 ENU08496 ANI61S2314: 70548	GTBX	CALc06228	2.1E-21	
24702 ENU08497 ANI61S3044: 78524	GTBX	CALc05604	6E-28	
24703 ENU08498 ANI61C3211: 11022301	GTBX	"AFUc19019, FGRc18454, Y13138"	"1.4e-48, 1.4e-29, 5.3e-	
24704 ENU08499 ANI61C3214: 5671777	GTBX	"AFUc19711, AFUc21339"	"8.6e-54, 5.8e-35"	
24705 ENU08500 ANI61C3215: 39465307	GTBX	"AFUc12382, AFUc15610"	"2.2e-89, 6.9e-46"	
24706 ENU08501 ANI61C3217: 15042206	GTBX	"AFUc13189, AFUc21901"	"9.0e- 158, 9.1e-10"	
24707 ENU08502 ANI61S2328: 554315	GTBX	"AFUc10225, Z71257"	"1.5e-14, 7.1e-55"	
24708 ENU08503 ANI61C3226: 78593	GTBX	"AFUc08295, AFUc08295"	"1.9e-41, 7.2e-37"	
24709 ENU08504 ANI61C2503: 11191520	GTBX	"FGRc05378, FGRc11560"	"8.0e-32, 7.5e-31"	

# ngungan maare

ption												
% id cvrg Description												
											•	
Blast Prob "1.3e-75, 1.1e-16, 3.0e-61, 1.2e-51,	4.8E-29	"1.0e-27, 3.9e-66"	3.6E-41	1.2E-102	5E-33	2.2e-76	"7.2e-11, 2.8e-38, 3.1e-61, 2.3e-43, 1.5e-17"	3.6E-63	6.4E-124	3.6E-48	"4.4e-65, 7.4e-51"	1.4E-48
Blast e Score												
aat Score												
ncbi gi												
Database Hit "AFUc01811, AFUc13887, CALc04895, FGRc00754,	AFUc10571	"AFUc02726, AFUc04017"	AFUc04584	AFUc14282	CALc05093	257	"AFUc05446, AFUc08551, AFUc16108, AFUc20988, CALC01643"	CALc05636	CALc05278	AFUc14444	"AFUc15224, FGRc07913"	AFUc06140
	AFI	"AF			CA	Z71257	AFE AFE AFE	CA				
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos												
Primer 5 pos												
Contig source ANI61C3235: 591675	24711 ENU08506 ANI61C3236: 1660614	24712 ENU08507 ANI61C2507: 1225200	24713 ENU08508 ANI61C2508: 90665	24714 ENU08509 ANI61C2509: 1495683	ANI61C3238: 22743441	24716 ENU08511 ANIGLC1130 0:1611872	24717 ENU08512 ANI61C1130 1:1372796	ANI61C2510: 55549	ANI61C2511: 1515260	ANI61C2512: 41685	24721 ENU08516 ANI61C3245: 2214196	ANI61C1131 7:109887
Seq num Seq id 24710 ENU08505	ENU08506	ENU08507	ENU08508	ENU08509	24715 ENU08510 ANI61C323 22743441	ENU08511	ENU08512	24718 ENU08513 ANI61C251 55549	24719 ENU08514 ANI61C251 1515260	24720 ENU08515 ANI61C251 41685	ENU08516	24722 ENU08517 ANI61C113 7:109887
Seq num 24710	24711	24712	24713	24714	24715	24716	24717	24718	24719	24720	24721	24722

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Blast Blast % Score Prob % id cvrg Description 6E-34	4.6E-49	9.5e-39	2.6E-39	"2.1e-21, 2.0e-53, 2.9e-	1.4E-271	6.2E-38	"1.7e-46, 2.2e-30, 6.4e-	"9.3e-25, 8.8e-07"	"2.7e-25, 6.2e-23"	"1.3e-91, 7.4e-43"	8.3E-21	4.1E-39
aat E Score S												
Database Hit ncbi gi AFUc10385	AFUc13043	Y13140	AFUc10893	"AFUc02484, AFUc04329, AFUc14153"	AFUc15767	AFUc16517	"AFUc02688, AFUc15728, AFUc15728"	"AFUc14903, AFUc15880"	"CALc06147, FGRc12101"	"AFUc03068, FGRc11923"	FGRc25342	AFUc07909
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos												
Seq num Seq id Contig source 24723 ENU08518 ANI61S3085: 1474	24724 ENU08519 ANI61C3251: 27823157	24725 ENU08520 ANI61C3255: 27642980	24726 ENU08521 ANI61C1132 5:65341	24727 ENU08522 ANI61C1132 8:179319	24728 ENU08523 ANI61C3261: 27603156	24729 ENU08524 ANI61C3262: 51642	24730 ENU08525 ANI61C3264: 17382478	24731 ENU08526 ANI61C2538: 16453	24732 ENU08527 ANI61C1060 1:10122306	24733 ENU08528 ANI61C1060 2:1474542	24734 ENU08529 ANI61C1133 2:4693	24735 ENU08530 ANI61C1133 3:4193

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24736 ENU08531 ANI61C1060 5:7635	Selection Basis GTBX	Database Hit ncbi gi "AFUc09745, CALc06186"	aat Blast Blast % Score Score Prob % id cvrg Dt "7.8e-56, 1.0e-55"	Description
24737 ENU08532 ANI61C1133 6:88652	GTBX	AFUc15671	1.8E-77	
24738 ENU08533 ANI61C2540: 53867	GTBX	"AFUc14945, AFUc22252"	"2.1e-11, 1.6e-31"	
24739 ENU08534 ANIGICI811: 216464	GTBX	FGRc11239	2.3E-23	
24740 ENU08535 ANI61C2541: 3861450	GTBX	"AFUc03214, FGRc12435"	"2.1e- 101, 6.5e-10"	
24741 ENU08536 ANI61C3271: 6184	GTBX	AFUc10952	2.1E-36	
24742 ENU08537 ANI61C2544: 1425331	GTBX	"AFUc10649, AFUc12123"	"3.1e-51, 4.0e-17"	
24743 ENU08538 ANI61C3274: 23732881	GTBX	AFUc02920	4.4E-81	
24744 ENU08539 ANI61C3279: 16191183	GTBX	AFUc14951	8E-175	
24745 ENU08540 ANI61C1134 3:3311459	GTBX	"AFUc09854, AFUc09854"	"2.4e- 113, 2.9e-87"	
24746 ENU08541 ANI61C1061 5:1232399	GTBX	"AFUc18846, FGRc03863"	"5.5e-67, 4.5e-27"	
24747 ENU08542 ANI6IC1134 5:19521431	GTBX	AFUc14213	4.3E-49	
24748 ENU08543 ANI61C1134 6:1470487	GTBX	"AFUc00459, AFUc17980, AFUc18124, FGRc01734"	"1.5e-13, 1.6e-21, 3.9e-31, 1.8e-40"	

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Seq num Seq id 24749 ENU08544	Contig source ANI61C1061 7:2430444	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc02314, AFUc19482,	aat Blast Score Score	Blast Prob "4.9e-60, 1.5e-95,	% id cvrg Description
24750 ENU08545 ANI61C1134 8:28093127	ANI61C1134 8:28093127			GTBX	CALCOSZOS "AFUC13004, AFUC13004"		2.7c-01 "1.3e-41, 2.7e-27"	
24751 ENU08546 ANI61C1134 9:6701324	ANI61C1134 9:6701324			GTBX	AFUc14220		3.6E-114	
24752 ENU08547 ANI61C2550: 17202019	ANI61C2550: 17202019			GTBX	AFUc11380		6.6E-52	
24753 ENU08548 ANI61C1823: 41605	ANI61C1823: 41605			GTBX	"AFUc09877, AFUc09877"		"2.5e-95, 8.9e-	
24754 ENU08549 ANIGIC2554: 76816	ANI61C2554: 76816			GTBX	AFUc12616		1.9E-72	
24755 ENU08550 ANI61C2556: 66404	ANI61C2556: 66404			GTBX	AFUc14572		6E-30	
24756 ENU08551 ANI61C10 0:736361	ANI61C1062 0:736361			GTBX	AFUc03637		2E-45	
24757 ENU08552 ANI61C1135 2:18953234	ANI61C1135 2:18953234			GTBX	"AFUc03502, AFUc07772"		"3.4e-59, 3.2e-91"	
24758 ENU08553 ANI61S1661: 4452	ANI61S1661: 4452			GTBX	AFUc02010		2.3E-40	
24759 ENU08554 ANI61C1062 6:48105096	ANI61C1062 6:48105096			GTBX	"AFUc05250, CALc06081"		"2.6e-49, 2.4e-21"	
24760 ENU08555 ANI61C1135 6:3461950	ANI61C1135 6:3461950			GTBX	AFUc15510		9.1E-121	
24761 ENU08556 ANI61C1830: 318882	ANI61C1830: 318882			GTBX	AFUc10397		2.1E-122	
24762 ENU08557 ANI61C2562: 15302081	ANI61C2562: 15302081			GTBX	"CALc05470, CALc05792"		"2.5e-32, 1.7e-37"	

# coreco ospiono

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24763 ENU08558 ANIG1C2568: 24638	r Selection Basis GTBX	Database Hit ncbi gi AFUc05821	aat Blast Blast % Score Score Prob % id cvrg Description 1.1E-28
24764 ENU08559 ANI61C1839: 3301127	GTBX	"AFUc09025, AFUc11515"	"6.1e-41, 5.2e-77"
24765 ENU08560 ANI61C1063 0:46532	GTBX	AFUc05997	6.4E-30
24766 ENU08561 ANI61C1063 1:1861843	GTBX	"AFUc01713, AFUc05435, AFIT-05435"	"1.3e-63, 6.4e-41, 6.5e-55"
24767 ENU08562 ANI61C1840: 1346639	GTBX	AFUc18505	1.1E-37
24768 ENU08563 ANI61C1843: 115501	GTBX	FGRc11281	8.9E-46
24769 ENU08564 ANI61C1846: 2841741	GTBX	"FGRc02282, FGRc05940, FGRc11631"	"2.6e-23, 1.4e-13, 1.3e-09"
24770 ENU08565 ANI61C2577: 199920	GTBX	"CALc05069, FGRc17612"	"2.7e-41, 6.0e-44"
24771 ENU08566 ANI61C1064 1:17073655	GTBX	"AFUc11683, Y13135"	"3.3e- 190, 5.1e- 119"
24772 ENU08567 ANI61C1137 2:74894	GTBX	AFUc17844	3.7E-26
24773 ENU08568 ANI61C1064 5:47619	GTBX	AFUc21723	2E-68
24774 ENU08569 ANI61C2582: 54245048	GTBX	AFUc01594	1.5E-28
24775 ENU08570 ANI61C1856: 658141	GTBX	AFUc16536	3.5E-26
24776 ENU08571 ANI61C2588: 75422	GTBX	"AFUc08407, FGRc10457"	"4.6e-49, 6.6e-60"

Blast Blast %  e Score Prob % id cvrg Description 8.9E-77	5.9E-32	4.6E-27	3.8e-149	4.2E-84	6.6E-39	4.1E-47	3E-180	"9.1e-29, 1.8e-53"	1.4E-63	"3.6e-55, 0.0"	4.1E-44	2.6e-62	5.3E-23
n Database Hit ncbi gi Score AFUc13209	AFUc17037	FGRc08856	Y13135	CALc06050	AFUc03173	AFUc15731	AFUc14963	"AFUc17647, FGRc25036"	AFUc06633	"AFUc09935, Y13140"	AFUc10713	Y13135	AFUc02315
ner Selection os Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 5 24777 ENU08572 ANI61C2589: 1861330	24778 ENU08573 ANI61C1138 1:10811457	24779 ENU08574 ANI61C1138 3:624383	24780 ENU08575 ANI61C1065 4:78928920	24781 ENU08576 ANI61C1065 5:91254	24782 ENU08577 ANI61C1065 7:66666094	24783 ENU08578 ANI61C1138 8:62701	24784 ENU08579 ANI61C1861: 1870524	24785 ENU08580 ANI61C2592: 13633	24786 ENU08581 ANI61C1865: 15892224	24787 ENU08582 ANIGIC2594: 50021392	24788 ENU08583 ANI61C1866: 15681080	24789 ENU08584 ANI61C2599: 46072	24790 ENU08585 ANI61C1066 5:664406

# octor ceraine

aat Blast Blast % i Score Score Prob % id cvrg Description 1.1E-28	"3.1e-34, 1.1e-19"	3.2E-57	"1.2e-96, 2.3e- 121"	2.7E-50	8.3E-27	3.2E-94	"5.7e-30, 1.2e-14"	2.4E-63	"1.6e-82, 2.8e-14"	3.5E-30	1.1E-64	"1.5e-81, 1.0e-41,	"6.0e-55, 2.5e- 114"
n Database Hit ncbi gi AFUc22562	"AFUc01385, AFUc09613"	CALc03969	"AFUc15461, AFUc15461"	AFUc10889	AFUc11094	AFUc11192	"AFUc11110, Y13138"	AFUc12481	"AFUc04431, AFUc16451"	AFUc21307	AFUc10552	"AFUc11549, AFUc15367,	AFUC17813 "AFUC05242, AFUC10990"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 24791 ENU08586 ANI61C1139 5:30212575	24792 ENU08587 ANI61C1871: 26054	24793 ENU08588 ANI61C1067 3:9221413	24794 ENU08589 ANI61C1067 5:27191441	24795 ENU08590 ANI61C1067 5:34043889	24796 ENU08591 ANI61C1067 8:1080600	24797 ENU08592 ANI61C9002: 1846878	24798 ENU08593 ANI61C9004: 32353965	24799 ENU08594 ANI61C9008: 314861	24800 ENU08595 ANI61C1880: 721179	24801 ENU08596 ANI61C1883: 54619	24802 ENU08597 ANI61C1885: 102195	24803 ENU08598 ANI61C710:2 8051017	24804 ENU08599 ANI61C713:1 67074

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24805 ENU08600 ANI61C1068 3:14871242	Selection Basis GTBX	Database Hit ncbi gi AFUc13939	aat Blast Blast Score Score Prob 1.4E-22	% % id cvrg Description
24806 ENU08601 ANI61C1068 9:1065390	GTBX	"AFUc13250, FGRc13107"	"6.4e-93 1.4e-10"	
24807 ENU08602 ANI61C9015: 4051	GTBX	AFUc12921	3.1E-56	
24808 ENU08603 ANI61C1895: 23652	GTBX	AFUc10988	1.4E-60	
24809 ENU08604 ANI61C720:1 602685	GTBX	CALc06106	3.6E-78	
24810 ENU08605 ANI61C1069 5:865252	GTBX	AFUc10487	9.9E-50	
24811 ENU08606 ANI61C9025: 463194	GTBX	AFUc00949	5.1E-49	
24812 ENU08607 ANI61C8300: 800189	GTBX	"AFUc08390, AFUc13837"	"3.3e-41, 6.5e-22"	
24813 ENU08608 ANI61C9030: 108511	GTBX	"AFUc06221, CALc06213, V13134"	"8.3e-40, 2.3e-13, 4 6e-13"	<b>.</b>
24814 ENU08609 ANI61C9039: 57696530	GTBX	"AFUc00570, FGRc14945"	"3.4e-28, 2.5e-08"	
24815 ENU08610 ANI61C8310: 465181	GTBX	FGRc10180	3.2E-24	
24816 ENU08611 ANI61C8314: 27242023	GTBX	AFUc21917	5.4E-31	
24817 ENU08612 ANI61C9048: 611497	GTBX	"AFUc14050, FGRc03000"	"1.3e-98, 3.4e-28"	٠.٠
24818 ENU08613 ANI61C751:4 20749	GTBX	AFUc06278	1.4E-42	

Blast Blast % Score Prob % id cvrg Description "2.5e-72, 1.5e-27, 6.6e- 196, 7.1e- 126, 8.6e- 128, 3.7e-75, 2.9e-35"	"5.8e-26, 1.3e-23"	3.5E-37	1.8E-25	"8.7e-69, 1.6e-54"	4.4E-30	"1.4e-81, 1.8e- 100, 1.1e-08"	1.7E-35	"1.5e-11, 4.3e-09, 6.4e-29, 1.4e-79"	1.1E-58	"7.8e-21, 5.9e-61"
aat Score										
ncbi gi										
Database Hit "AFUc05783, AFUc12204, AFUc12677, CALC06075, FGRc11436,	"AFUc04172, FGRc02654"	AFUc12859	AFUc09750	"AFUc02770, AFUc09905"	AFUc09154	"AFUc13510, AFUc14636, FGRc04398"	AFUc09586	"AFUc09078, AFUc18318, FGRc07495,	AFUc01959	"AFUc04122, Y13139"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
3 pos										
Primer 5 pos										
Seq. num Seq id Contig source : 24819 ENU08614 ANI61C758:4 029103	24820 ENU08615 ANI61C8322: 16631077	24821 ENU08616 ANI61C8325: 79477	24822 ENU08617 ANI61C8326: 8601122	24823 ENU08618 ANI61C8330: 1999807	24824 ENU08619 ANI61C7605: 19391517	24825 ENU08620 ANI61C9063: 60604119	24826 ENU08621 ANI61C7606: 185886	24827 ENU08622 ANI61C9067: 40431889	24828 ENU08623 ANI61C770:7 8335	24829 ENU08624 ANI61C775:4 811025

# nound cario

Seq num Seq id 24830 ENU08625	Contig source ANI61C8340: 6001358	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc09848, FGRc00517"	aat Blast Blast Score Score Prob "2.6e" 1.0e-2	Blast % Prob % id cvrg Description 2.6e-41, 1.0e-27"
24831 ENU08626 ANI61C7615: 53558	ANI61C7615: 53558			GTBX	AFUc01625	3.5E-52	-52
24832 ENU08627 ANI61C7616: 31662391	ANI61C7616: 31662391			GTBX	"AFUc00961, FGRc05631"	"1.7 5.5e	"1.7e-25, 5.5e-16"
24833 ENU08628 ANI61C7617: 102082	ANI61C7617: 102082			GTBX	"AFUc13516, CALc04464"	"1.8 9.5e	"1.8e-84, 9.5e-47"
24834 ENU08629 ANI61C7618: 449192	ANI61C7618: 449192			GTBX	AFUc12936	6.3E-53	-53
24835 ENU08630 ANI61C9077: 618241	ANI61C9077: 618241			GTBX	AFUc02355	2.6E-33	-33
24836 ENU08631 ANI61C8348: 15622188	ANI61C8348: 15622188			GTBX	AFUc06232	1.9	1.9E-58
24837 ENU08632 ANI61C9078: 28671238	ANI61C9078: 28671238			GTBX	"CALc05373, FGRc09215, FGRc14791, Y13140"	"1.3e- 1.3e-2 1.1e-4 9.9e- 187"	"1.3e-93, 1.3e-21, 1.1e-43, 9.9e-
24838 ENU08633 ANI61C7 461	ANI61C780:4 461			GTBX	"AFUc13983, Y13137"	"2.6" "2.6 4.3e	"2.6e-42, 4.3e-33"
24839 ENU08634 ANI61C7 3979	ANI61C781:6 3979			GTBX	AFUc10848	5.4E-43	-43
24840 ENU08635 ANI61C7 0222710	ANI61C789:4 0222710			GTBX	"AFUc16570, AFUc17384"	1.9	"1.9e-52, 1.0e-67"
24841 ENU08636 ANI61C8350: 27424517	ANI61C8350: 27424517			GTBX	CALc06237	2.9I	2.9E-46
24842 ENU08637 ANI61C9080: 2749969	ANI61C9080: 2749969		•	GTBX	"AFUc07425, AFUc19355"	"3.7 1.2e	"3.7e-17, 1.2e-21"

% % id cvrg Description													
Blast Prob 7.9E-64	"3.9e-65, 1.1e-30"	"1.4e-08, 1.3e-11,	2.5E-28	1.8E-38	5.6E-29	"3.4e-18, 2.0e-68"	"2.2e-36, 9.8e-13"	1.1E-46	"5.9e-50, 3.4e-47, 1.0e-46, 3.3e-44"	"7.9e-30, 1.3e-62"	2E-80	5E-68	"3.5e-77, 2.4e-13"
aat Blast Score Score													
Database Hit ncbi gi AFUc15938	"AFUc12206, Y13140"	"AFUc01781, AFUc01807,	CALc06163	AFUc20257	AFUc15667	"AFUc12939, AFUc14002"	"AFUc10758, AFUc10988"	AFUc01337	"AFUc15806, AFUc22456, FGRc02315,	"AFUc15550, U00092"	AFUc11236	AFUc11952	"AFUc09758, CALc05309"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq Contiguence 1 Contiguence 24843 ENU08638 ANIGIC9082: 251958	24844 ENU08639 ANI61C8354: 1395895	24845 ENU08640 ANI61C8355: 5512115	24846 ENU08641 ANI61C7628: 3290	24847 ENU08642 ANI61C792:6 85317	24848 ENU08643 ANI61C794:1 079852	24849 ENU08644 ANI61C797:1 5212941	24850 ENU08645 ANI61C798:5 4814	24851 ENU08646 ANI61C7633: 311964	24852 ENU08647 ANI61C8363: 4971386	24853 ENU08648 ANI61C9092: 1981162	24854 ENU08649 ANI61C6908: 658381	24855 ENU08650 ANI61C6910: 1381152	24856 ENU08651 ANI61C8372: 8701638

aat Blast % Score Score Prob % id cvrg Description "2.3e-91, 1.3e-40"	3.6E-35	3.9E-25	1.5E-24	"2.6e-31, 2.0e-36"	1.3E-46	"1.8e-65, 5.3e-67"	3.1E-59	3.6E-44	1.2E-51	5.1E-41	"2.0e-43, 1.1e-20"	"7.7e-34, 4.4e-29"	"2.1e-66, 1.2e-50, 4.0e-37"
Selection Basis Database Hit ncbi gi GTBX "AFUc05629, AFUc21466"	GTBX AFUc14464	GTBX AFUc18416	GTBX CALc05557	GTBX "AFUc04661, AFUc22181"	GTBX AFUc01242	GTBX "AFUc03128, AFUc07465"	GTBX AFUc09509	GTBX AFUc07723	GTBX AFUc03234	GTBX AFUc08515	GTBX "AFUc02256, AFUc08836"	GTBX "AFUc07074, AFUc11027"	GTBX "CALc05819, FGRc11819, FGRc11819"
Seq Primer Primer Sinum Seq id Contig source 5 pos 3 pos B 24857 ENU08652 ANIG1C8375: G	24858 ENU08653 ANIGIC6919: G 239529	24859 ENU08654 ANI61C7649: G 949566	24860 ENU08655 ANIGIC7651: G 78670	24861 ENU08656 ANI61C6925: G	24862 ENU08657 ANI61C6926: G 6921049	24863 ENU08658 ANIGIC6927: G 35352135	24864 ENU08659 ANI61C8385: G 30043390	24865 ENU08660 ANI61C6930: G 909328	24866 ENU08661 ANI61C6931: G	24867 ENU08662 ANIG1C7661: G	24868 ENU08663 ANI61C8391: C	24869 ENU08664 ANI61C7663: C	24870 ENU08665 ANI61C7664: C 6201668

Seq num Seq id 24871 ENU08666	Contig source ANI61C7665: 14051690	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc20344, FGRc25908"	aat Blast Score Score	Blast Prob "3.0e-52, 9.4e-22"	% id cvrg Description	c
24872 ENU08667 ANIGIC7667: 217764	ANI61C7667: 217764			GTBX	AFUc15868		2.8E-59		
24873 ENU08668 ANI61C 54621	ANI61C7668: 54621			GTBX	AFUc19926		1.1E-48		
24874 ENU08669 ANI61C7669: 1362145	ANI61C7669: 1362145			GTBX	"AFUc16122, AFUc18675, CAL <sub>C</sub> 06209"		"6.4e-69, 4.8e-37, 4.3e-96"		
24875 ENU08670 ANI61C8398: 12561657	ANI61C8398: 12561657			GTBX	"CALc03932, FGRc14057, FGRc23953"		"4.4e- 108, 2.3e-24, 2.2e-44"		
24876 ENU08671 ANI61C6941: 27701688	ANI61C6941: 27701688			GTBX	CALc06022		4E-79		
24877 ENU08672	ANI61C6942: 1015337			GTBX	"AFUc09643, FGRc10423"		"9.0e-22, 6.3e-13"		
24878 ENU08673 ANI61C7672: 41495074	ANI61C7672: 41495074			GTBX	AFUc15338		2.1E-67		
24879 ENU08674 ANI61C7673: 27063490	ANI61C7673: 27063490			GTBX	U00094		4.6e-253		
24880 ENU08675 ANI61C7675: 75886036	ANI61C7675: 75886036			GTBX	"AFUc09612, AFUc18486"		"8.0e-40, 1.4e-39"		
24881 ENU08676 ANI61C6948: 514290	ANI61C6948: 514290			GTBX	AFUc14750		2.7E-34		
24882 ENU08677 ANI61C7689: 2240860	ANI61C7689: 2240860			GTBX	AFUc07888		4.6E-109		
24883 ENU08678 ANI61C 5146	ANI61C10:13 5146			GTBX	AFUc04257		9.9E-80		
24884 ENU08679 ANI61C18:28 740	ANI61C18:28 740			GTBX	AFUc06457		1.5E-24		

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Seq num Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Blast Score Score	Blast Prob	% % id cvrg Description
24885 ENU08680 ANI61C6964: 2636	ANI61C6964: 2636			GTBX	AFUc19698		1.6E-27	
24886 ENU08681 ANI61C7695: 12053	ANI61C7695: 12053			GTBX	"AFUc14143, FGRc21455"		"2.4e-80, 1.1e-26"	
24887 ENU08682 ANI61C6967: 687361	ANI61C6967: 687361			GTBX	"AFUc15762, AFUc15762"		"1.8e-68, 3.0e- 170"	
24888 ENU08683 ANI61C6968: 222943	ANI61C6968: 222943			GTBX	"AFUc08123, CALc05688"		"6.6e-24, 5.1e-87"	
24889 ENU08684 ANI61C6969: 14971	ANI61C6969: 14971			GTBX	AFUc08629		1.1E-84	
24890 ENU08685 ANI61C21:10 21690	ANI61C21:10 21690			GTBX	"FGRc05811, U00094"		"1.1e-51, 1.2e-97"	
24891 ENU08686 ANI61C24:13 02541	ANI61C24:13 02541			GTBX	AFUc10888		2.2E-38	
24892 ENU08687 ANI61C27:13 601941	ANI61C27:13 601941			GTBX	CALc04049		5.6E-149	
24893 ENU08688 ANI61C29:12 4077	ANI61C29:12 4077			GTBX	U00094		2.0e-29	
24894 ENU08689 ANI61C6974: 15121835	ANI61C6974: 15121835			GTBX	"AFUc12767, FGRc04567"		"1.8e-09, 1.4e-32"	
24895 ENU08690 ANI61C6976: 78011	ANI61C6976: 78011			GTBX	AFUc20643		5.4E-33	
24896 ENU08691 ANI61C6978: 936477	ANI61C6978: 936477			GTBX	FGRc17293		5E-24	
24897 ENU08692 ANI61C6979: 20072660	ANI61C6979: 20072660			GTBX	AFUc14080		3.3E-22	
24898 ENU08693 ANI61C4002: 1132302	ANI61C4002: 1132302			GTBX	AFUc10817		4.7E-59	

## oecen cention

Blast Blast %  e Score Prob % id cvrg Description "3.5e-56, 6.5e-48, 5.2e-50, 1.7e-24"	4.6E-33	1.2e-31	"4.7e-19, 2.8e-36"	1.2E-52	1.2E-45	1.5E-77	3.1E-39	8E-28	1.7E-28	1.8E-23	"9.0e-24, 2.0e-21, 2.6e-33"	6.1E-33	3.8E-40
Database Hit ncbi gi Score "AFUc10260, FGRc02884, FGRc12117, FGRc12117,	AFUc00656	Y13135	"FGRc11412, FGRc17886"	AFUc12892	AFUc15961	AFUc15151	AFUc13524	AFUc15217	AFUc00826	AFUc09449	"AFUc07978, FGRc00983, FGRc23299"	AFUc12810	FGRc12892
Primer Primer Selection 5 pos 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq num Seq id Contig source 5 j 24899 ENU08694 ANI61C34:77 82349	24900 ENU08695 ANI61C36:77 634	24901 ENU08696 ANI61C6980: 3631007	24902 ENU08697 ANI61C6985: 6255	24903 ENU08698 ANI61C6986: 1531763	24904 ENU08699 ANI61C40:84 11771	24905 ENU08700 ANI61C46:92 8116	24906 ENU08701 ANI61S645:4 1428	24907 ENU08702 ANI61C6999: 887135	24908 ENU08703 ANI61C4021: 103714	24909 ENU08704 ANI61C55:10 16.1329	24910 ENU08705 ANI61C61:65 604412	24911 ENU08706 ANI61C61:96 648595	24912 ENU08707 ANI61C4034: 490254

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24913 ENU08708 ANI61C3307: 9971236	r Selection Basis GTBX	Database Hit ncbi gi AFUc14556	aat Blast Blast Score Score Prob 7.7E-33	% id cvrg Description
24914 ENU08709 ANI61C3309: 35901383	GTBX	"AFUc19897, CALc05545, FGRc10593"	"3.7e-34, 9.3e- 107, 6.2e-41"	
24915 ENU08710 ANI61S3148: 132339	GTBX	U00094	3.86-13	
24916 ENU08711 ANI61C70:15 41477	GTBX	AFUc13679	3.1E-42	
24917 ENU08712 ANI61C74:20 411277	GTBX	"FGRc02814, FGRc10359, FGRc18356"	"6.6e-59, 2.0e-50, 1.3e-07"	
24918 ENU08713 ANI61C3315: 10211941	GTBX	AFUc14821	6.4E-117	
24919 ENU08714 ANI61C3317: 43174820	GTBX	AFUc11811	1E-69	
24920 ENU08715 ANI61C4046: 9442324	GTBX	AFUc09421	3.9E-37	
24921 ENU08716 ANI61C4047: 816382	GTBX	AFUc02478	2.6E-45	
24922 ENU08717 ANI61C81:39 812518	GTBX	AFUc10625	3E-101	
24923 ENU08718 ANI61C3322: 44749	GTBX	AFUc19143	1.4E-21	
24924 ENU08719 ANI61C3323: 50654721	GTBX	AFUc13265	1.3E-49	
24925 ENU08720 ANI61C84:12 67794	GTBX	CALc05272	2.5E-47	
24926 ENU08721 ANI61C3328: 10492	GTBX	Y13136	2.9e-49	

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Seq num Seq id Contig source 24941 ENU08736 ANI61C4072. 1036572	Contig source ANI61C4072: 1036572	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit nc AFUc03577	a ncbi gi S	aat Blast Score Score	Blast Prob 8.2E-78	% id cvrg Description
24942 ENU08737 ANI61C2615: 4272074	ANI61C2615: 4272074			GTBX	"AFUc19837, Y13138"			"2.6e-44, 1.4e-41"	
24943 ENU08738 ANI61C3344: 172816	ANI61C3344: 172816			GTBX	FGRc02406			5.1E-25	
24944 ENU08739 ANI61C2616: 8202283	ANI61C2616: 8202283			GTBX	"AFUc05687, AFUc08664, CALc05800,			"1.7e-49, 7.9e-07, 1.9e-35, 8 4e-26"	
24945 ENU08740 ANI61C4074: 249872	ANI61C4074: 249872			GTBX	"FGRc11944, U00092"			"4.4e-70, 4.4e-36"	
24946 ENU08741 ANI61C4076: 30557	ANI61C4076: 30557			GTBX	"AFUc13132, FGRc02840"			"6.1e-32, 2.0e-09"	
24947 ENU08742 ANI61C1141 5:2205964	ANI61C1141 5:2205964			GTBX	"AFUc09709, AFUc12435"			"1.5e-66, 6.1e-81"	
24948 ENU08743 ANI61C4080: 37961	ANI61C4080: 37961			GTBX	AFUc07865			6.1E-73	
24949 ENU08744 ANI61C4082: 632399	ANI61C4082: 632399			GTBX	AFUc11950			1.1E-26	
24950 ENU08745 ANI61C3355: 6191088	ANI61C3355: 6191088			GTBX	AFUc10222			1.5E-54	
24951 ENU08746 ANI61C3356: 976367	ANI61C3356: 976367			GTBX	AFUc12958			1.1E-81	
24952 ENU08747 ANI61C3358: 47656066	ANI61C3358: 47656066			GTBX	AFUc15520			3.1E-70	
24953 ENU08748 ANI61C3359: 1074440	ANI61C3359: 1074440			GTBX	AFUc13793			4.5E-78	
24954 ENU08749 ANI6IC1142 2:67466	ANI61C1142 2:67466			GTBX	AFUc07909			2.1E-36	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24955 ENU08750 ANI61C1142 3:7481	Selection Basis GTBX	, , ,	% id cvrg	Description
ANI61C) 7:38702	GTBX	"AFUc08441, FGRc23451, Y13140"	"6.1e-07, 4.6e-12, 4.6e-41"	
24957 ENU08752 ANI61C1142 9:1930573	GTBX	AFUc06257	1.6E-22	
24958 ENU08753 ANI61C2630: 541105	GTBX	AFUc08424	3.4E-59	
24959 ENU08754 ANI61C2633: 26252233	GTBX	AFUc05841	3.1E-54	
24960 ENU08755 ANI61C4093: 33385	GTBX	AFUc04043	3.8E-27	
24961 ENU08756 ANI61C2636: 1040489	GTBX	AFUc11267	4.1E-79	
24962 ENU08757 ANI61C1909: 1484	GTBX	AFUc13018	2.2E-63	
24963 ENU08758 ANI61C4098: 14842175	GTBX	"AFUc12633, AFUc13482, CALc05318"	"5.9e-20, 3.8e-68, 1.2e-10"	
24964 ENU08759 ANI61C1070 0:57866253	GTBX	AFUc10021	2.9E-39	
24965 ENU08760 ANI61C1143 0:4991727	GTBX	AFUc11277	1.9E-64	
24966 ENU08761 ANI61C1143 2:33083949	GTBX	"AFUc16152, AFUc16297"	"7.7e-15, 4.1e-26"	
24967 ENU08762 ANI61C1070 4:902062	GTBX	"AFUc03602, AFUc18530"	"2.2e-36, 4.7e-60"	
24968 ENU08763 ANI61C1143 5:3451916	GTBX	"AFUc05782, AFUc15229, FGRc13683"	"1.4e- 122, 2.6e-09, 2.4e-37"	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24969 ENU08764 ANI61C1070 6:961211235	Selection Basis GTBX	Database Hit ncbi gi "AFUc07945, AFUc12767,	aat Blast Blast % Score Score Prob % id cvrg Description "2.3e-24, 5.9e-12, 5.7e-66"
24970 ENU08765 ANI61C1143 6:87068281	GTBX	FGRc12034	1.2E-21
24971 ENU08766 ANI61C1070 7:9481825	GTBX	"AFUc11321, AFUc14716,	"6.5e-95, 1.7e-40, 5.5e.00"
24972 ENU08767 ANI61C1070 9:111425	GTBX	AFUc09791	5.5E-28
24973 ENU08768 ANI61C1910: 4071	GTBX	AFUc15581	8.3E-33
24974 ENU08769 ANI61C1912: 1407133	GTBX	"AFUc08239, FGRc26694"	"1.1e-64, 1.4e-38"
24975 ENU08770 ANI61C3371: 1098181	GTBX	AFUc05453	4.4E-22
24976 ENU08771 ANI61C1913: 2846.474	GTBX	"CALc05504, U00094"	"1.5e-77, 1.8e-11"
24977 ENU08772 ANI61C3372: 682993	GTBX	AFUc14289	7.5E-43
24978 ENU08773 ANI61C1915: 22162827	GTBX	AFUc16313	1.2E-50
24979 ENU08774 ANI61C3376: 1445891	GTBX	AFUc12472	3.7E-45
24980 ENU08775 ANI61C2647: 36452	GTBX	AFUc00608	6.1E-35
24981 ENU08776 ANI61C1919: 77319	GTBX	U00094	1.3e-87
24982 ENU08777 ANIGIC3378: 12162	GTBX	AFUc10430	2.9E-166

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Seq num Seq id 24983 ENU08778	Contig source ANI61C1071 3:17283141	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc05029, FGRc10887"	aat Blast Blast Score Score Prob "1.9e-28,	% % id cvrg Description 8,
24984 ENU08779 ANI61C1144 4:43435216	ANI61C1144 4:43435216			GTBX	"AFUc08298, AFUc22104"	"3.9e-17, 1.2e-23"	7,
24985 ENU08780 ANI61C1071 6:32191252	6:32191252			GTBX	"AFUc09877, AFUc11768, FGR-03217"	"6.4e-52, 4.4e-81, 3.6e-26"	·
24986 ENU08781 ANI61C2 1167676	ANI61C2651: 1167676			GTBX	AFUc06429	1.4E-47	
24987 ENU08782 ANI61C2 670338	ANI61C2653: 670338			GTBX	FGRc07112	4.2E-45	10
24988 ENU08783	ANI61C2654: 8231444			GTBX	Y13138	2.9e-38	
24989 ENU08784 ANI61C2 2061236	ANI61C2656: 20612360			GTBX	FGRc02646	6.5E-25	S.
24990 ENU08785 ANI61C1 1654734	ANI61C1928: 1654734			GTBX	AFUc12945	5.9E-109	60
24991 ENU08786 ANI61C3388: 95417	ANI61C3388: 95417			GTBX	AFUc08509	2.9E-47	7
24992 ENU08787 ANI61C1 0:56584	ANI61C1072 0:56584			GTBX	AFUc06323	6.2E-26	9
24993 ENU08788 ANI61C1 1:22721	3 ANI61C1072 1:22721494			GTBX	AFUc12398	7.6E-75	S
24994 ENU08789 ANI61C1 2:56216	2:5621611			GTBX	"AFUc15498, AFUc18421"	"4.6e- 113, 7.1e-50"	-
24995 ENU08790 ANI61S1 76593	) ANI61S1767: 76593			GTBX	AFUc10191	9.3E-93	3
24996 ENU08791 ANI61C1930: 1036686	ANI61C1930: 1036686			GTBX	CALc06119	1.1E-69	6

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 24997 ENU08792 ANI61C1931: 353729	Selection Basis GTBX	Database Hit ncbi gi AFUc14831	aat Blast Blast Score Score Prob 3.1E-80	% % id cvrg Description 80
24998 ENU08793 ANI61C2660: 11151436	GTBX	"AFUc12566, AFUc14338"	"7.5e-40, 3.9e-35"	-40, 35"
24999 ENU08794 ANIGIC1933: 16131178	GTBX	AFUc07117	3.2E-66	99-
25000 ENU08795 ANI61C3397: 30911810	GTBX	"AFUc11193, AFUc11193, FGRc03055"	"1.4e-43, 1.4e-59, 8.1e-12"	-43, 59, 12"
25001 ENU08796 ANI61C1073 7:13252336	GTBX	"AFUc18885, CALC04126, V13140"	"3.5e-44, 1.8e-25, 9.6e-35"	25, 35"
25002 ENU08797 ANIG1C1146 7:385858	GTBX	AFUc19804	3.5E-37	37
25003 ENU08798 ANI61C1146 7:28601414	GTBX	"AFUc09725, CALc06090"	"7.7e-53, 2.6e-08"	≻53, 08"
25004 ENU08799 ANI61C1941: 1051823	GTBX	"CALc05195, FGRc16068, V13138"	"2.7e-31, 1.7e-37, 2.1e-97"	≻31, 37, 97"
25005 ENU08800 ANI61C2670: 1338683	GTBX	"AFUc08344, FGRc03704"	"2.7e-31, 3.7e- 101"	×31,
25006 ENU08801 ANI61C1943: 20484	GTBX	AFUc11732	1.9E-76	-76
25007 ENU08802 ANI61C2673: 76930	GTBX	"AFUc13809, CALc05583"	"3.6e-71, 1.4e-64"	≻71, 64"
25008 ENU08803 ANI61C1946: 6473	GTBX	FGRc10049	8.7E-42	-42
25009 ENU08804 ANI61C2676: 1204362	GTBX	AFUc13919	6.5E-148	-148
25010 ENU08805 ANI61C2679: 18532069	GTBX	Y13138	2.4e-23	23

Blast % Prob % id cvrg Description "2.7e-56, 2.1e-23"	1.9E-80	IE-25	1.9E-43	6.3E-198	"4.9e- 131, 9 1e-41"	8.4E-87	IE-44	4.6E-32	1.5E-24	1.8E-26	2.8E-128	1.8E-45	"6.5e-27, 4.2e-61"
aat Blast E Score Score F	1	1	1	9	. 1	ν ∞	-	4	-	_	7	_	: 4
Database Hit ncbi gi "AFUc10091, FGRc03364"	AFUc14682	AFUc03516	AFUc06521	AFUc14969	"AFUc14718, FGRc15556"	AFUc14883	AFUc14574	AFUc11691	AFUc15229	AFUc04303	AFUc09746	AFUc13804	"AFUc07690, AFUc12854"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 25011 ENU08806 ANI61C1074 0:91922	25012 ENU08807 ANI61C1074 1:1607918	25013 ENU08808 ANI61C1147 1:21641046	25014 ENU08809 ANI61C1074 2:19082430	25015 ENU08810 ANI61C1147 8:12922764	25016 ENU08811 ANI61C1952: 21853687	25017 ENU08812 ANI61C1957: 14671747	25018 ENU08813 ANI61C1075 0:15892369	25019 ENU08814 ANI61C1148 1:48235	25020 ENU08815 ANI61C1075 3:141476	25021 ENU08816 ANI61C1960: 18711443	25022 ENU08817 ANI61C2692: 34282316	25023 ENU08818 ANI61C2693: 44995	25024 ENU08819 ANI61C2698: 745259

u													
% id cvrg Description													
% cvrg D													
pi %											•		•
Blast Prob "2.8e-25, 4.2e-61,	"2.6e-24, 2.2e-25"	3.5E-85	8.1e-21	8.6E-34	2.7E-47	"1.2e-72, 7.4e-92, 9.9e-72, 1.3e-13"	1.3E-23	9.8E-56	2.3E-87	4.6E-54	"9.0e-27, 1.5e-26"	3.2E-57	"5.8e-55, 5.9e-42"
Blast Score													
aat Score													
Hit ncl 190, 54,		4		47	53	768, 38, 91,	. 03	51	8	83	588, 92"	81	126, 62"
Database Hit ncbi gi "AFUc09690, AFUc12854, FGR c07517"	"CALc05408 FGRc05636"	AFUc11524	Z47047	AFUc15874	AFUc14463	"AFUc11768, AFUc14088, AFUc14691, FGRc19856"	FGRc08860	AFUc15761	AFUc14848	AFUc10383	"AFUc03688, FGRc07492"	AFUc05381	"AFUc13126, FGRc07962"
uo													
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos													
Primer 5 pos													
	21076 109	21076 .3500	C1972:	C1973:	C1974:	C1975:	C807:1	C809:3	C1077 5669	C9100:	C9104:	C9105: 501	C9107:
Contig source ANI61C2698: 1594988	ANI61C107 4:709109	ANI61C1076 7:24753500	ANI61C1 1158691	ANI61C) 128544	ANI61C) 196552	ANI61C 27206	ANI610 04363	ANI61C8 97740	ANI61C1077 6:47645669	ANI61C9 1569543	ANI61C910 50435687	ANI61C9 1952601	ANI61C91( 36605664
Seq num Seq id Contig source 25025 ENU08820 ANI61C2698: 1594988	25026 ENU08821 ANI61C1076 4:709109	25027 ENU08822 ANI61C1076 7:24753500	25028 ENU08823 ANI61C1 1158691	25029 ENU08824 ANI61CI 128544	25030 ENU08825 ANI61C1974: 196552	25031 ENU08826 ANI61C1 27206	25032 ENU08827 ANI61C807:1 04363	25033 ENU08828	25034 ENU08829 ANI61C1077 6:47645669	25035 ENU08830 ANI61C9100: 1569543	25036 ENU08831 ANI61C9104: 50435687	25037 ENU08832 ANI61C9105: 1952601	25038 ENU08833 ANI61C9107: 36605664
Seq id SENU08	6 EN	7 ENT	28 ENT	9 ENI	SO ENT	31 ENT	32 ENT	33 EN	34 ENI	35 EN	36 ENI	37 ENI	38 EN
Seq num 2502	2502	2502	2502	2502	2503	2503	2503	2503	2503	2503	250	250.	250.

aat Blast Blast % Score Score Prob % id cvrg Description 4.6E-41	3.1E-28	3.1E-114	7.5E-81	1.9E-60	4.9E-54	"3.3e-67, 4.0e-15"	2.IE-37	"1.3e-44, 1.5e-19"	"2.2e-62, 5.0e-45"	1.4E-38	"1.9e-40, 7.0e-35"	"4.2e- 100, 7.6e- 120"	2E-36
Database Hit ncbi gi FGRc24873	FGRc09740	AFUc13090	AFUc05724	AFUc12748	AFUc22177	"AFUc05152, AFUc06401"	AFUc05328	"AFUc06686, AFUc11073"	"AFUc12162, AFUc19854"	AFUc02177	"AFUc03882, FGRc06121"	"AFUc04821, Y13138"	AFUc12750
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 25039 ENU08834 ANI61C818:3 2562912	25040 ENU08835 ANI61C1078 8:151949	25041 ENU08836 ANI61C1078 9:18961027	25042 ENU08837 ANI61C9112: 22153174	25043 ENU08838 ANI61C9112: 47943825	25044 ENU08839 ANI61C9117: 46505342	25045 ENU08840 ANI61C9118: 24814081	25046 ENU08841 ANI61C822:9 78138	25047 ENU08842 ANI61C826:4 551470	25048 ENU08843 ANI61C827:1 03074	25049 ENU08844 ANI61C828:2 3242715	25050 ENU08845 ANI61C1079 2:295726	25051 ENU08846 ANI61C1079 6:176438	25052 ENU08847 ANI61C9125: 1139627

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Seq num Seq id 25053 ENU08848	Seq id Contig source ENU08848 ANI61C836:8 95335	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc14883, AFUc14883"	aat Blast Score Score	Blast Prob "5.8e-46, 7.5e-53"	% id cvrg Description	Description
25054 ENU08849 ANI61C 1566	ANI61C837:4 1566			GTBX	AFUc20588		3.6E-38		
25055 ENU08850 ANI61C8403: 22651942	ANI61C8403: 22651942			GTBX	AFUc08360		7.3E-22		
25056 ENU08851 ANI61C8406: 33831653	ANI61C8406: 33831653			GTBX	"AFUc12104, AFUc15297, V13135"		"4.0e-62, 3.7e-23, 3.0e-46"		
25057 ENU08852 ANI61C9136: 666908	ANI61C9136: 666908			GTBX	AFUc13948		5.9E-32		
25058 ENU08853 ANI61C8407: 2066705	ANI61C8407: 2066705			GTBX	"AFUc13751, AFUc13751"		"3.4e- 186, 6.1e- 210"		
25059 ENU08854 ANI61C 328231	ANI61C848:1 328.2315			GTBX	AFUc08609		1.7E-86		
25060 ENU08855 ANI61C 739232	ANI61C8411: 7392328			GTBX	"CALc05880, D50617"		"3.4e-96, 2.2e-48"		
25061 ENU08856 ANI61C 181111	ANI61C8413: 18111191			GTBX	"AFUc07925, Y13139"		"1.6e- 105, 2.0e-95"		
25062 ENU08857 ANI61C8414: 791278	ANI61C8414: 791278			GTBX	"AFUc01427, FGRc11796"		"1.1e-07, 3.1e-73"		
25063 ENU08858 ANI61C8418: 15591860	ANI61C8418: 15591860			GTBX	AFUc13723		3.3E-33		
25064 ENU08859 ANI61C8419: 14512381	ANI61C8419: 14512381			GTBX	"AFUc08249, FGRc12401"		"2.7e- 159, 1 8e_23"		
25065 ENU08860 ANI61C9149: 27582324	ANI61C9149: 27582324			GTBX	AFUc02271		1.4E-50		

Blast Blast % Score Prob % id cvrg Description 3.6E-28	9.4E-77	"2.8e-34, 1.4e-22"	4.9E-55	1.8E-45	1.4E-68	2.2e-20	"4.3e-21, 7.0e-54, 4.0e-20"	3.6E-34	1.3E-50	1.3E-83	1.6E-70	6.9e-17	2.8E-24
aat Bl. Score Sc													
Database Hit ncbi gi FGRc06929	AFUc12396	"AFUc12828, FGRc08325"	AFUc21112	AFUc10496	AFUc09889	Y13135	"AFUc11864, AFUc13604, AFIC15296"	FGRc20146	AFUc14422	AFUc12944	FGRc12224	Y13135	FGRc12904
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 25066 ENU08861 ANI61C851:1 0291701	25067 ENU08862 ANI61C853:7 641566	25068 ENU08863 ANI61C855:7 0519	25069 ENU08864 ANI61C857:2 3641240	25070 ENU08865 ANI61C9154: 108330	25071 ENU08866 ANI61C8429: 16391370	25072 ENU08867 ANI61C867:9	25073 ENU08868 ANI61C7703: 1506530	25074 ENU08869 ANI61C7704: 1011306	25075 ENU08870 ANI61C8433: 3374	25076 ENU08871 ANI61C8436: 13971989	25077 ENU08872 ANI61C7709: 812115	25078 ENU08873 ANI61C875:2 0571446	25079 ENU08874 ANI61C8441: 1416541

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25080 ENU08875 ANI61C7714:	Selection Basis GTBX	Database Hit ncbi gi "FGRc06342, FGRc14811"	aat Blast Blast Score Score Prob % "8.4e-13, 6.0e-22"	% id cvrg Description
25081 ENU08876 ANI61C8446: 62029	GTBX	"AFUc11909, FGRc12199"	"3.5e-19, 7.9e-38"	
25082 ENU08877 ANI61C7717: 11131711	GTBX	AFUc07025	3.2E-41	
25083 ENU08878 ANI61C7717: 59815119	GTBX	"AFUc16351, FGRc04611"	"4.4e-23, 7.7e-20"	
25084 ENU08879 ANI61C9179: 38905546	GTBX	"AFUc13046, AFUc22205"	"7.7e-96, 9.1e-37"	
25085 ENU08880 ANI61C886:5 2243674	GTBX	"AFUc04165, AFUc14221"	"5.2e-09, 9.9e-39"	
25086 ENU08881 ANI61C888:4 2223713	GTBX	AFUc20805	2.2E-28	
25087 ENU08882 ANI61C7721: 5631320	GTBX	"AFUc12977, AFUc14414"	"6.6e-33, 6.6e-17"	
25088 ENU08883 ANI61C7724: 45794	GTBX	AFUc10173	3.6E-116	
25089 ENU08884 ANI61C8456: 212740	GTBX	"AFUc09795, Z71256"	"7.6e-59, 6.7e- 21?"	
25090 ENU08885 ANI61C9189: 1464940	GTBX	AFUc00837	8.5E-38	
25091 ENU08886 ANI61C894:1 514653	GTBX	AFUc15628	4.7E-69	
25092 ENU08887 ANI61C9190: 1512525	GTBX	"FGRc00983, FGRc26079"	"3.9e-44, 5.8e-18"	
25093 ENU08888 ANI61C8463: 8151153	GTBX	AFUc11295	5.4E-117	

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aat Blast Blast % t ncbi gi Score Score Prob % id cvrg Description 5.3E-40	4.5E-41	), "2.0e-29, 1.8e-29,		2.3E-27	0, "3.2e-58, " 3.5e-11"	1.1E-22	9, "1.9e-19, 1.5e-38, " 6.9e-		3, "7.8e-60, " 1.4e-15"	2, "1.9e- " 102, 3 9e-98"		1.6E-33
Database Hit AFUc12028	FGRc25728	"AFUc05790, AFUc13990,	FGRc13634	AFUc09614	"AFUc18110, FGRc17629"	AFUc02394	"AFUc13489, AFUc17708, CALc05924"	AFUc21062	"CALc05253, FGRc26927"	"AFUc12062, AFUc14671"	AFUc15656	CALc04035
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
sr Primer 3 pos												
Primer 5 pos		\ <del>``</del>	÷		ä	::	<u></u>	::	.;;	.;;	7:	÷.
Seq id Contig source ENU08889 ANI61C7735: 367666	ANI61C7736: 25516	ANI61C9196 5091774	ANI61C7739 947600	ANI61C9198 816496	ANI61C8469 1100398	ANI61C847( 1108629	ANI61C7741 25224541	ANI61C8475 7311763	ANI61C7756 1266573	ANI61C8486 27393881	ANI61C8487 2372427	ANI61C7759
Seq num Seq id 25094 ENU08889	25095 ENU08890 ANI61C 25516	25096 ENU08891 ANI61C9196: 5091774	25097 ENU08892 ANI61C7739: 947600	25098 ENU08893 ANI61C9198: 816496	25099 ENU08894 ANI61C8469: 1100398	25100 ENU08895 ANI61C8470: 1108629	25101 ENU08896 ANI61C7741: 25224541	25102 ENU08897 ANI61C8475: 7311763	25103 ENU08898 ANI61C7756: 1266573	25104 ENU08899 ANI61C8486: 27393881	25105 ENU08900 ANI61C8487: 2372427	25106 ENU08901 ANI61C7759.

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Seq         Primer         Primer           num         Seq id         Contig source         5 pos         3 pos           25107         ENU08902         ANI61C8490:         3 pos           25108         ENU08903         ANI61C7762:         5841           25110         ENU08904         ANI61C7765:         76357           25111         ENU08905         ANI61C776:         86706           25112         ENU08907         ANI61C776:         86706           25113         ENU08909         ANI61C7770:         98979           25114         ENU08910         ANI61C7771:         88264           25115         ENU08911         ANI61C7771:         88264           25115         ENU08911         ANI61C7771:         88264           25115         ENU08911         ANI61C7771:         3631698           25117         ENU08912         ANI61C7774:         36572305           25118         ENU08913         ANI61C7777:         10631767	Selection Basis GTBX GTBX GTBX GTBX GTBX GTBX GTBX GTBX	Database Hit ncbi gi "CALC05635, FGRc06214, FGRc20613" AFUc10277  Z71256  AFUc21500  AFUc21500  AFUc03608  "FGRc00672, FGRc09713" "AFUc01209, AFUc02171, FGRc0050" AFUc01162 "AFUc05844, FGRc12412"	Score Score	Blast Prob "9.5e-66, 4.0e-20, 9.4e-68" 6E-91 7.6e-26 2.9E-46 1.9E-112 1.9E-112 1.9E-112 3.9e-37" "4.0e-28, 3.9e-16" "3.1e-32, 3.4e-14" 5.6E-121	% id cvrg Description
25119 ENU08914 ANI61C7786: 232921	GTBX	AFUc05158		3.6E-50	
25120 ENU08915 ANI61C7789: 7351117	GTBX	AFUc14811		7.1E-29	

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Seq num Seq id 25121 ENU08916	Seq id Contig source ENU08916 ANI61S719:4 58168	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc05321	aat Blast I Score Score I	Blast Prob 1E-29	% % id cvrg Description
25122 ENU08917 ANI61C7792: 2071448	ANI61C7792: 2071448			GTBX	"AFUc15949, FGRc07097"		"3.3e-38, 7.1e-24"	
25123 ENU08918 ANI61C4102: 15851031	ANI61C4102: 15851031			GTBX	AFUc14601		9.8E-63	
25124 ENU08919 ANI61C 891301	ANI61C4103: 891301			GTBX	"AFUc02035, AFUc18244, FGRc16341"		"6.8e-16, 6.3e-49, 1.0e-12"	
25125 ENU08920 ANI61C4106: 8881172	ANI61C4106: 8881172			GTBX	AFUc12497		6.4E-29	
25126 ENU08921 ANI61C4107: 30734246	ANI61C4107: 30734246			GTBX	"AFUc03644, AFUc03949, AFUc07144"		"2.3e-51, 1.8e-29, 3.7e-22"	
25127 ENU08922 ANI61C4107: 68484563	ANI61C4107: 68484563			GTBX	"AFUC10284, AFUC16568, FGRc23371"		"3.4e- 124, 1.8e-25, 4.3e-10"	
25128 ENU08923 ANI61C4108: 10562837	ANI61C4108: 10562837			GTBX	"AFUc05077, AFUc15554, FGRc08841"		2.6e-43, 5.2e- 121, 4.0e-59"	
25129 ENU08924 ANI61S .352	ANI61S51:11. .352			GTBX	AFUc09974		4.7E-50	
25130 ENU08925 ANI61C4116: 565195	ANI61C4116: 565195			GTBX	"AFUc14805, AFUc20877"		"6.4e-36, 4.6e-38"	
25131 ENU08926 ANI61C4119: 741313	ANI61C4119: 741313			GTBX	AFUc06070		1E-39	
25132 ENU08927 ANI61C4124: 24822991	ANI61C4124: 24822991			GTBX	AFUc11634		4.7E-39	

Blast Blast %  e Score Prob % id cvrg Description "3.5e- 270, 7.0e-28, 3.2e- 273"	3.2E-59	7.8E-23	"1.5e-56, 2.4e-60"	"1.5e-37, 1.6e-95"	1.2E-68	"1.2e-26, 2.2e-14, 4.4e-21, 6.2e-23"	5.5E-26	3.5E-33	"4.1e-10, 3.8e-30"	7.6E-67	2E-23	6.6E-32
aat Score												
ncbi gi ),			~ ·	~~~ -		<b>o</b> *			<u>بر</u> -			
Database Hit ncbi gi "AFUc14940, FGRc02042, U00094"	AFUc15050	AFUc08654	"CALc06080, CALc06080"	"AFUc19418, FGRc07284"	AFUc04164	"AFUc01839 AFUc16911, AFUc22154, EGRc12232"	AFUc20668	AFUc11116	"AFUc21598, FGRc22967"	AFUc15424	AFUc05316	AFUc04175
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos												
Primer 5 pos												
Seq num Seq id Contig source 25133 ENU08928 ANI61C4126: 9783417	25134 ENU08929 ANI61S75:57 825	25135 ENU08930 ANI61C3400: 994518	25136 ENU08931 ANI61C3402: 1027517	25137 ENU08932 ANI61C4132: 27823311	25138 ENU08933 ANIGIC4134: 4951116	25139 ENU08934 ANI61C3406: 2435654	25140 ENU08935 ANI61C3409: 255582	25141 ENU08936 ANI61C4139: 107824	25142 ENU08937 ANIGIC4143: 51749	25143 ENU08938 ANI61C4145: 47552	25144 ENU08939 ANI61C3416: 15451820	25145 ENU08940 ANI61S772:2 7949

Blast % Prob % id cvrg Description 5.1E-38	1.2E-32	2.8E-33	"2.2e-72, 2.1e-26"	5.7E-114	3.6E-86	3.1E-21	1.4E-68	<b>4</b> =	3.1E-33	4.5E-52	8.6E-70	7.1E-95	1.4E-46
	1.2F	2.81	"2.2 2.1e	5.7E	3.6	3.11	1.4	"3.4e- 148, 5.7e- 208"	3.11	4.5	8.6	7.11	1.4
aat Blast Score Score													
ncbi gi													
Database Hit FGRc08165	AFUc14425	AFUc01911	"AFUc07502, CALc06043"	AFUc05660	AFUc08088	AFUc06449	AFUc06662	"AFUc15654, AFUc15654"	AFUc04760	AFUc06724	AFUc15132	AFUc15688	CALc05920
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
ner Primer													
Primer rce 5 pos .54:	126:	156:	164: 5	165:	t39:	8:2.	:72:	<del>14</del> 2:	:+44	:77:	723:	724:	726:
Contig source ANI61C4154: 750427	ANI61C34 7991035	ANI61C41 811158	ANI61C416	ANI61C416 28792147	ANI61C34 1918547	, ANI61S79 .358	ANI61S32 1396	ANI61C34	ANI61C34 1126196	ANI61C41 6221022	2913	875213	1 ANI61C27 57430
Seq num Seq id 25146 ENU08941	25147 ENU08942 ANI61C3426: 7991035	25148 ENU08943 ANI61C4156: 811158	25149 ENU08944 ANI61C4164: 11022126	25150 ENU08945 ANI61C4165: 2879.2147	25151 ENU08946 ANI61C3439: 1918547	25152 ENU08947 ANI61S798:2 .358	25153 ENU08948 ANI61S3272: 1396	25154 ENU08949 ANI61C3442: 9782365	25155 ENU08950 ANI61C3444: 1126196	25156 ENU08951 ANIGLC4177: 6221022	25157 ENU08952 ANI61C2723: 2913	25158 ENU08953 ANI61C2724: 875213	25159 ENU08954 ANI61C2726: 57430
Seq num 25146	25147	25148	25149	2515(	2515.	2515;	2515.	25154	2515:	2515	2515′	2515	2515

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aat Blast Blast % Score Score Prob % id cvrg Description 1.2E-83	4.9E-42	4.2E-60	1.1E-29	1.9E-63	2.8E-35	2E-109	"1.6e-11, 2.8e-64"	6.1E-56	5.6E-91	"6.1e-15, 1.5e-33"	6.5E-35	"9.6e-15, 1.4e-57"	"3.6e-08,
on Database Hit ncbi gi AFUc14608	: AFUc10128	: AFUc12576	: FGRc00578	C AFUc11038	; FGRc24279	. AFUc13761	. "AFUc00703, AFUc13932"	. AFUc07701	C AFUc11252	Z71257"	K AFUc01658	K "AFUc07431, AFUc13621"	<pre>CALC01138, CALC03518"</pre>
Primer Primer Selection 5 pos 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq num Seq id Contig source 5 25160 ENU08955 ANI61C4187: 3791145	25161 ENU08956 ANI61C3458: 1001567	25162 ENU08957 ANI61C3459: 669199	25163 ENU08958 ANI61S1831: 53219	25164 ENU08959 ANI61S1834: 390665	25165 ENU08960 ANI61S2569: 41484	25166 ENU08961 ANI61C3460: 10171299	25167 ENU08962 ANI61C3461: 84964	25168 ENU08963 ANI61C4191: 1298198	25169 ENU08964 ANI61C4195: 13871874	25170 ENU08965 ANI61C2738: 853278	25171 ENU08966 ANI61C4198: 582151	25172 ENU08967 ANI61C1080 6:191656	25173 ENU08968 ANI61C1080 7:54576306

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Seq num Seq id 25174 ENU08969	Seq id Contig source ENU08969 ANI61C3470: 13881606	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc07764	aat Blast gi Score Score	Blast % Prob % id cvrg Description 9.6E-105	sscription
25175 ENU08970 ANI61C3473: 772392	ANI61C3473: 772392			GTBX	AFUc18497		6.7E-24	
25176 ENU08971 ANI61C3475: 32093995	ANI61C3475: 32093995			GTBX	AFUc05872		9.5E-50	
25177 ENU08972 ANI61C2747: 43471	ANI61C2747: 43471			GTBX	AFUc14390		2.1E-34	
25178 ENU08973 ANI61C1081 2:15443776	ANI61C1081 2:15443776			GTBX	"AFUc13531, AFUc14233, AFUc14327, AFIC14338"		"3.9e-29, 2.4e-31, 9.0e-57, 3.8e-50"	
25179 ENU08974 ANI61C1081 4:545141	ANI61C1081 4:545141			GTBX	"AFUc09407, FGRc11267"		"3.5e-23, 4.1e-07"	
25180 ENU08975	ANI61S1855: 51573			GTBX	AFUc14395		7.2E-32	
25181 ENU08976 ANI61C2753: 7131036	ANI61C2753: 7131036			GTBX	AFUc12177		4.6E-28	
25182 ENU08977 ANI61C3482: 11591505	ANI61C3482: 11591505			GTBX	"AFUc08947, Y13137"		"3.6e-76, 2.1e-44"	
25183 ENU08978 ANI61C2754: 1520	ANI61C2754: 1520			GTBX	AFUc11200		1.1E-29	
25184 ENU08979 ANI61C3487: 3341136	ANI61C3487: 3341136			GTBX	AFUc21091		1.2E-22	
25185 ENU08980 ANI61C2758: 96608	ANI61C2758: 96608			GTBX	FGRc12220		7.4E-48	
25186 ENU08981 ANI61C2763: 1297582	ANI61C2763: 1297582			GTBX	"AFUc13692, AFUc13754"		"5.8e-77, 4.6e-43"	
25187 ENU08982 ANI61C3497: 38559	ANI61C3497: 38559			GTBX	FGRc10471		6.1E-74	

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t Blast % e Prob % id cvrg Description "1.8e- 106,	8.8E-23	1.5E-26	"9.0e- 161, 5.3e-60, 5.3e-	"8.3e-21, 1.3e-24"	4.5E-54	1.3E-97	2.6E-38	1.2E-34	5.2E-35	2.7E-43	5.7E-82	"1.0e-29, 1.0e-37"
Blast e Score												
aat Score												
ncbi gi												
Database Hit "AFUc14311, AFUc22325"	09165	15294	"AFUc14245, CALc05322, Y13140"	"AFUc21087, CALc06090"	AFUc10042	AFUc08854	AFUc14237	AFUc16118	AFUc13519	AFUc14105	AFUc13456	"AFUc12779, AFUc12779"
	AFUc09165	AFUc15294	"AFUc14 CALc053 Y13140"	"AFU CALC	AFUc	AFUc	AFUc	AFUc	AFUc	AFUc	AFUc	"AFU AFUc
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos												
Primer 5 pos												
Seq num Seq id Contig source 25188 ENU08983 ANI61C1083 6:2079834	25189 ENU08984 ANI61C2777: 24927	25190 ENU08985 ANI61C1084 2:26321	25191 ENU08986 ANI61C1084 6:22343543	25192 ENU08987 ANI61C1084 8:4163	25193 ENU08988 ANI61C1084 9:35484105	25194 ENU08989 ANI61C2783: 12712181	25195 ENU08990 ANI61C2791: 906498	25196 ENU08991 ANI61C2792: 87636	25197 ENU08992 ANI61C2794: 15841084	25198 ENU08993 ANI61C2799: 13201669	25199 ENU08994 ANI61C1086 2:1103489	25200 ENU08995 ANI61C1086 9:1089200

st Blast % re Prob % id cvrg Description "1.9e- 159, 5.5e-	"1.5e-46, 2.0e-50"	1.1E-83	"1.9e-69, 7.3e-13, 3.3e-27"	1.4E-33	7.5E-42	"1.1e-32, 4.6e-40, 5.1e-48, 1.4e-22"	IE-27	"1.7e- 141, 2.8e-29, 4 fe-48"	"9.2e-51, 2.8e-29, 2.3e-35"	6.2E-58	"3.1e-51, 9.2e-42"	9.1E-26
aat Blast Score Score												
Database Hit ncbi gi "CALc05217, Y13138"	"CALc03654, X59720"	AFUc15811	"AFUc04817, AFUc21485, FGR.c09205"	AFUc15632	AFUc08928	"AFUc09601, AFUc13531, AFUc15132, AFIC19875"	AFUc08110	"AFUc15140, AFUc15140, AFUc19221"	"AFUc09101, CALc01241, FGB_07803"	AFUCI1011	"AFUc14615, AFUc22530"	AFUc00720
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos												
Seq num Seq id Contig source 25201 ENU08996 ANI61C1087 2:20042818	25202 ENU08997 ANI6IC1087 3:11552865	25203 ENU08998 ANI61C1087 4:35654204	25204 ENU08999 ANI61C1087 5:822501	25205 ENU09000 ANI61C9200: 14232081	25206 ENU09001 ANI61C9201: 617383	25207 ENU09002 ANI61C9203: 452063	25208 ENU09003 ANI61C9206: 77081	25209 ENU09004 ANI61C9207: 35701397	25210 ENU09005 ANI61C914:4 5043529	25211 ENU09006 ANI61C918:1 531052	25212 ENU09007 ANI61C9211: 23953456	25213 ENU09008 ANI61C9215: 14941788

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Seq num Seq id 25214 ENU09009	Contig source ANI61C9216: 27551219	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc14313, AFUc14313"	aat Blast Score Score	Blast Prob "1.1e- 11.6e-	% % id cvrg Description
25215 ENU09010 ANI61C923:6 85239	ANI61C923:6 85239			GTBX	FGRc06929		157" 5.2E-27	
25216 ENU09011 ANI61C1089 2:25981435	ANI61C1089 2:25981435			GTBX	"AFUc03032, AFUc05892, V13140"		"4.4e-43, 5.3e-16, 5.4e-18"	
25217 ENU09012 ANI61C9227: 491215	ANI61C9227: 491215			GTBX	"AFUc09616, FGRc06065"		7.75-15 "3.1e- 106,	
25218 ENU09013 ANI61C9229: 44629	ANT61C9229: 44629			GTBX	AFUc20770		1.3E-32	
25219 ENU09014 ANI61C931:4 3321795	ANI61C931:4 3321795			GTBX	"AFUc06172, AFUc06611"		"6.7e-29, 3.0e-41"	
25220 ENU09015 ANI61C8503: 41764553	ANI61C8503: 41764553			GTBX	FGRc01667		2.7E-21	
25221 ENU09016 ANI61C8508: 10082044	ANI61C8508: 10082044			GTBX	"AFUc11315, CALc04402"		"7.7e-85, 4.4e-53"	
25222 ENU09017 ANI61C9237: 2822495	ANI61C9237: 2822495			GTBX	Y13134		8.0e-80	
25223 ENU09018 ANI61C948:1 06598	ANI61C948:1 06598			GTBX	AFUc19097		3.3E-34	
25224 ENU09019 ANI61C9240: 174861	ANI61C9240: 174861			GTBX	"AFUc15932, AFUc15932"		"2.9e-38, 3.7e-47"	
25225 ENU09020 ANI61C 892413	ANI61C8511: 892413			GTBX	AFUc13528		8E-52	
25226 ENU09021 ANI61C 55635	ANI61C8517: 55635			GTBX	FGRc00709		6.1E-30	
25227 ENU09022 ANI61C9247: 25931793	ANI61C9247: 25931793			GTBX	AFUc01187		2.4E-29	

Seq num Seq id 25228 ENU09023	Contig source ANI61C8519: 1036209	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc11611	aat Blast Score Score	Blast Prob 6E-54	% % id cvrg Description
25229 ENU09024 ANI61C953:9	ANI61C953:9 121			GTBX	AFUc13929		4.2E-68	
25230 ENU09025 ANI61C957:2 2627	ANI61C957:2 2627			GTBX	AFUc14610		1.8E-80	
25231 ENU09026 ANI61C8522: 21711635	ANI61C8522: 21711635			GTBX	AFUc02919		2.5E-49	
25232 ENU09027 ANI61C9253: 2222333	ANI61C9253: 22223333			GTBX	"AFUc05780, FGRc20446"		"1.4e-15, 3.6e-23"	
25233 ENU09028 ANI61C8526: 84165	ANI61C8526: 84165			GTBX	"AFUc09020, Y13136"		"2.0e-41, 7.5e-31"	
25234 ENU09029 ANI61C8526: 46175334	ANI61C8526: 46175334			GTBX	"AFUc21180, CALc04630"		"4.4e-40, 8.5e-22"	
25235 ENU09030 ANI61C9257: 1241480	ANI61C9257: 1241480			GTBX	CALc05995		1.4E-53	
25236 ENU09031 ANI61C8531: 35773233	ANI61C8531: 35773233			GTBX	AFUc07659		2.6E-27	
25237 ENU09032 ANI61C8533: 25491044	ANI61C8533: 25491044			GTBX	AFUc06933		8.6E-41	
25238 ENU09033 ANI61C9265: 83518701	ANI61C9265: 83518701			GTBX	AFUc13733		2.4E-119	
25239 ENU09034 ANI61C7807: 752321	ANI61C7807: 752321			GTBX	AFUc15441		2.4E-34	
25240 ENU09035 ANI61C 07278	ANI61C973:6 07278			GTBX	FGRc18829		6.4E-22	
25241 ENU09036 ANI61C975:7 0.423	ANI61C975:7 0423	_		GTBX	AFUc04456		3.4E-33	

Blast % Prob % id cvrg Description "1.9e-31, 1.3e-67"	"3.5e-45, 8.0e-26"	-31	-11	"7.4e-51, 9.7e-18, 3.9e-26"	"2.6e-82, 1.1e-30, 3.1e-12"	"1.2e-08, 1.9e-31"	"2.4e-80, 3.7e-25, 5.1e-25"	3.3E-134	"2.1e-21, 4.5e-77"	74	4.8E-30	"1.7e-83, 6.6e-23"	"8.4e-56, 4.2e-83"
	"3.5 8.0e	7.5E-31	2.9e-11	"7.4e-51 9.7e-18, 3.9e-26"	"2.6 1.1e 3.1e	"1.2 1.9e	3.7e	3.31	"2.1 4.5e	SE-74	4.81	1.7	4.26
Blast Score													
aat Score													
Database Hit ncbi gi "AFUc08733, AFUc10087"	2805, 089"	158		2018, 483, 778"	2368, 695, 695"	3289, 872"	7632, 753, 461"	752	8206, 826"	633	523	8217, 703"	5765, 1653"
Database Hit "AFUc08733 AFUc10087"	"AFUc02805, AFUc21089"	AFUc16158	U00092	"AFUc02018, AFUc15483, AFUc15778"	"AFUc12368, AFUc15695, AFUc15695"	"AFUc03289 AFUc12872"	"AFUc07632, AFUc16753, CALc05461"	AFUc15752	"AFUc08206, AFUc13826"	AFUc13633	FGRc02523	"AFUc08217 FGRc09703"	"AFUc15765, CALc05653"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos													
Primer 5 pos													
ource 976:5	25243 ENU09038 ANI61C978:7 6118	ANI61C8542: 2313	25245 ENU09040 ANI61C7814: 22792073	25246 ENU09041 ANI61C8544: 62307238	25247 ENU09042 ANI61C7817: 209338	25248 ENU09043 ANI61C8547: 22442879	25249 ENU09044 ANI61C7825: 1907493	25250 ENU09045 ANIGIC7827: 166912	25251 ENU09046 ANI61C992:2 8503833	25252 ENU09047 ANI61C8562: 871199	25253 ENU09048 ANI61C8565: 6371002	25254 ENU09049 ANI61C9295: 1450440	25255 ENU09050 ANI61C8566: 77039
Seq id Contig s 2 ENU09037 ANI61C 01755	3 ENU09038	25244 ENU09039 ANI61C 2313	5 ENU09040	6 ENU09041	7 ENU09042	8 ENU09043	9 ENU09044	0 ENU09045	1 ENU09046	2 ENU09047	3 ENU09048	4 ENU09049	5 ENU09050
Seq num 25242	2524	2524	2524	2524	2524	2524	2524	2525	2525	2525	2525	2525	2525

aat Blast Blast % Score Score Prob % id cvrg Description 4.1E-61	"5.1e-25, 5.2e-74"	"3.5e-38, 3.5e-49"	3.5E-112	"3.7e-79, 6.3e-13"	"1.6e-61, 1.1e-32"	"5.3e-29, 1.9e-21"	8.9E-30	2.3e-12	1.4E-123	5.1E-49	5.9E-22	"3.9e-21, 3.2e-20"	"1.4e-13, 8.8e-21, 2.0e- 143"
Selection Basis Database Hit ncbi gi GTBX AFUc03216	3X "AFUc14355, AFUc22510"	BX "AFUc00708, AFUc09276"	BX AFUc15765	BX "AFUc06883, FGRc14811"	BX "AFUc10607, U00094"	BX "AFUc03724, FGRc24839"	BX AFUc06423	BX Y13140	BX AFUc12170	BX AFUc19366	BX AFUc02328	BX "AFUc03531, AFUc12810"	BX "AFUc03147, CALc06221, Z71257"
Primer Selecti 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq Primer num Seq id Contig source 5 pos 25256 ENU09051 ANI61C8568: 111968	25257 ENU09052 ANI61C9298: 81518	25258 ENU09053 ANI61C9299: 6571844	25259 ENU09054 ANI61C7844: 946392	25260 ENU09055 ANI61C8574: 16012681	25261 ENU09056 ANI61C7847: 9312031	25262 ENU09057 ANI61C7849: 43324955	25263 ENU09058 ANI61C8580: 1023210627	25264 ENU09059 ANI61C8584: 101535	25265 ENU09060 ANI61C7855: 29204065	25266 ENU09061 ANI61C7855: 65074837	25267 ENU09062 ANI61C7857: 4881039	25268 ENU09063 ANI61C7864: 30453936	25269 ENU09064 ANI61C8596: 20922

## cette ce e e e e e e e e e

Sed		Primer	Primer	Selection		aat Blast Blast	%
num Seq id Contig source 25270 ENU09065 ANI61S4000: 4726	Contig source ANI61S4000: 4726	sod s	3 pos	Basis GTBX	Database Hit ncbi gi "AFUc15463, Y13135"	re Score	% id cvrg Description 32,
25271 ENU09066 ANI61C7872: 891147	ANI61C7872: 891147			GTBX	AFUc15367	1.3E-32	32
25272 ENU09067 ANI61C7875: 4433500	ANI61C7875: 4433500			GTBX	"AFUc05240, AFUc12411, FGRc05490, FGRc06942, FGRc06942,	"1.8e-11, 8.3e-53, 1.1e-98, 1.5e-15, 2.0e-14,	.11, 53, 98, 15, 14,
25273 ENU09068 ANI61C7878: 277566	ANI61C7878: 277566			GTBX	FGRc14988	1.5E-32	32
25274 ENU09069 ANI61C7879: 719118	ANI61C7879: 719118			GTBX	FGRc09098	1.6E-29	29
25275 ENU09070 ANI61C7886: 5805	ANI61C7886: 5805			GTBX	"AFUc04118, AFUc11270"	"1.6e-44, 2.6e-34"	-44, 34"
25276 ENU09071 ANI61C7892: 13421082	ANI61C7892: 13421082			GTBX	AFUc02446	1.9E-36	36
25277 ENU09072 ANI61C7896: 21702465	ANI61C7896: 21702465			GTBX	CALc05565	2E-23	
25278 ENU09073 ANI61C7899: 58735220	ANI61C7899: 58735220			GTBX	CALc02982	1.2E-79	97
25279 ENU09074 ANI61C4200: 725149	ANI61C4200: 725149			GTBX	FGRc08664	5.3E-52	52
25280 ENU09075 ANI61C4203: 1767622	ANI61C4203: 1767622			GTBX	"AFUc01235, AFUc07012"	"1.0e-61, 9.5e-19"	-61, 19"
25281 ENU09076 ANI61C4208: 34415	ANI61C4208: 34415			GTBX	AFUc14843	1.1E-38	38
25282 ENU09077 ANI61C4212: 6018	ANI61C4212: 6018			GTBX	FGRc13621	2.6E-48	48

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Seq num Seq id 25283 ENU09078	Contig source ANI61C4212: 11342468	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi Y13134	aat Blast Score Score	Blast Prob 2.1e-68	% id cvrg Description
25284 ENU09079 ANI61C4216: 49115121	ANI61C4216: 49115121			GTBX	AFUc03988		2.2E-35	
25285 ENU09080 ANIGIC4219: 2071864	ANI61C4219: 2071864			GTBX	AFUc13992		2.4E-190	
25286 ENU09081 ANI61C4223: 1637692	ANI61C4223: 1637692			GTBX	AFUc14306		1.8E-91	
25287 ENU09082 ANI61C4224: 1911741	ANI61C4224: 1911741			GTBX	"CALc03890, Y13135"		"4.2e-60, 1.9e-76"	
25288 ENU09083 ANI61C4233: 31134950	ANI61C4233: 31134950			GTBX	"AFUc01615, AFUc12868, AFUc20678, AFUc22517"		"1.0e-31, 2.9e-24, 4.2e-56, 2.5e-13"	
25289 ENU09084 ANI61C4234: 13311654	ANI61C4234: 13311654			GTBX	AFUc03297		2.IE-31	
25290 ENU09085 ANI61C3508: 817356	ANI61C3508: 817356			GTBX	FGRc06621		2.9E-35	
25291 ENU09086 ANI61C3509: 157516	ANI61C3509: 157516			GTBX	CALc04641		4.5E-178	
25292 ENU09087 ANI61S2616: 50511	ANI61S2616: 50511			GTBX	AFUc06531		6.2E-27	
25293 ENU09088 ANI61C3511: 79819	ANI61C3511: 79819			GTBX	"AFUc06952, AFUc11209, AFIIc13557"		"3.5e-13, 2.2e-18, 8.2e-54"	
25294 ENU09089 ANI61S878:1 9522	ANI61S878:1 9522			GTBX	FGRc06247		2.1E-46	
25295 ENU09090 ANI61C4254. 841526	ANI61C4254: 841526			GTBX	AFUc14249		2.6E-57	
25296 ENU09091 ANI61C3528: 308516	ANI61C3528: 308516			GTBX	CALc04521		9.2E-30	

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Seq num Seq id 25297 ENU09092	Contig source ANI61C4258: 25161242	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc12040, CALc05713"	aat Blast Blast Score Score Prob "2.7e- 192,	% id cvrg Description
25298 ENU09093 ANI61C4260: 17396	ANI61C4260: 17396			GTBX	"AFUc03360, FGRc19992"	7.0e-37 "6.2e-57, 1.2e-13"	57, 3".
25299 ENU09094 ANI61C2802: 1479234	ANI61C2802: 1479234			GTBX	U00094	4.1e-78	8.
25300 ENU09095 ANI61C3532: 49627	ANI61C3532: 49627			GTBX	AFUc05925	8.1E-31	31
25301 ENU09096 ANI61C2803 56868	ANI61C2803: 56868			GTBX	FGRc09627	1E-65	
25302 ENU09097 ANI61C3534: 24221935	ANI61C3534: 24221935			GTBX	CALc03078	1.9E-32	32
25303 ENU09098 ANI61C2806: 9691276	ANI61C2806: 9691276			GTBX	AFUc12155	5.3E-37	37
25304 ENU09099 ANI61S898:1 63579	ANI61S898:1 63579			GTBX	AFUc09587	2.8E-60	09
25305 ENU09100 ANI61C3540: 514302	ANI61C3540: 514302			GTBX	FGRc16169	3.5E-24	24
25306 ENU09101	ANI61C4278: 22981835			GTBX	FGRc24333	3E-34	
25307 ENU09102 ANI61C4278: 2825.4111	ANI61C4278: 28254111			GTBX	"AFUc06051, FGRc18955"	"2.3e-08, 8.1e-33"	.08, 33"
25308 ENU09103 ANI61C4280: 1451765	ANI61C4280: 1451765			GTBX	"AFUc13963, FGRc19878"	"6.5e-20, 1.4e-35"	20, 35"
25309 ENU09104 ANI61C2825: 1042103	ANI61C2825: 1042103			GTBX	AFUc09268	1.8E-72	27
25310 ENU09105 ANI61C4283: 21422672	ANI61C4283: 21422672			GTBX	AFUc12329	4.3E-48	48

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25311 ENU09106 ANI61C4285: 27044107 25312 ENU09107 ANI61C3557: 107924 1507913	Selection Basis GTBX GTBX GTBX	Database Hit ncbi gi AFUc07246 AFUc13932 "FGRc09765, Y13135"	aat Blast Blast % Score Score Prob % id cvrg Description 3.2E-153 2.7E-33 "7.1e-33, 3.2e-53"	Description
25314 ENU09109 ANI61C2834: 1324253 25315 ENU09110 ANI61C3565: 801109	GTBX	"AFUc14023, AFUc18413, FGRc11244" "AFUc12638, AFUc14019"	"2.3e-36, 1.6e-52, 8.8e-07" "3.6e-94, 1.7e-19"	
25316 ENU09111 ANI61C2836: 8421150 25317 ENU09112 ANI61C4295:	GTBX	AFUc09693 "AFUc14660,	3.9E-47 "2.9e-12,	
5262590 25318 ENU09113 ANI61C3569: 22474	GTBX	AFUc15941, AFUc15941" AFUc01238	4.1e-55, 6.5e-45" 1.1E-22	
25319 ENU09114 ANI61C1090 0:246490 25320 ENU09115 ANI61C1090 1:24497	GTBX	FGRc11747 AFUc13935	9.5E-32 3.6E-65	
25321 ENU09116 ANI61C3570: 6071650 25322 ENU09117 ANI61C3578:	GTBX	"CALc05316, U00094" AFUc04929	"2.9e-10, 1.1e-41" 9.7E-23	
68364 25323 ENU09118 ANI61C1091 2:864129	GTBX	AFUc15752	1.8E-26	
25324 ENU09119 ANI61C1091 6:1704605	GTBX	AFUc14099	1.1E-29	

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% % id cvrg Description													
Blast Prob "3.9e-33, 3.7e-94, 6.7e-58"	6.3E-23	1.1E-37	1.5E-30	8.9E-30	1.3E-39	7.9E-57	5.3E-59	1.2E-23	6.3E-54	4.4E-62	1.7E-30	"1.2e-23, 2.8e-09"	"1.1e-81, 1.6e-60, 1.3e-56, 6.3e-08"
Blast Score													
aat Score													
ncbi gi													
Database Hit "AFUc10454, AFUc14364, CALc03886"	AFUc09771	CALc06129	AFUc17615	AFUc14337	FGRc08083	FGRc01600	AFUc01539	FGRc05834	AFUc06319	AFUc09790	AFUc09609	"AFUc16521, AFUc16612"	"AFUc16639, FGRc02861, FGRc09286, FGRc11948"
e o													
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos													
Primer 5 pos													•
Seq num Seq id Contig source 25325 ENU09120 ANI61C2852: 17221	25326 ENU09121 ANI61C3582: 1760305	25327 ENU09122 ANI61C2856: 623366	25328 ENU09123 ANI61C3587: 576272	25329 ENU09124 ANI61C1092 7:60324	25330 ENU09125 ANI61S2694: 35812	25331 ENU09126 ANI61C2860: 743120	25332 ENU09127 ANI61C3590: 22121250	25333 ENU09128 ANIGIC2864: 234450	25334 ENU09129 ANI61C2866: 4002	25335 ENU09130 ANI61C3596: 5088	25336 ENU09131 ANI61C1093 1:14581075	25337 ENU09132 ANI61C1093 2:26741592	25338 ENU09133 ANI61C1093 4:2128413

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Seq Primer Primer Primer Seq id Contig source 5 pos 3   25339 ENU09134 ANI61C1093   7:18362395	Primer So 3 pos B G	Selection Basis GTBX	Database Hit ncbi gi AFUc04964	aat Blast Bl Score Score Pr 1.	Blast % Prob % id cvrg Description 1.3E-86
25340 ENU09135 ANI61C1094 6:1623629	9	GTBX	"AFUc07110, AFUc18195"	1.0	"6.0e-77, 1.6e-11"
25341 ENU09136 ANI61C2889: 806204	9	GTBX	AFUc12218	5.0	5.6E-93
25342 ENU09137 ANI61C1095 4:25793314	5	GTBX	Y13139	71	1.7e-39
25343 ENU09138 ANI61C1095 5:53242	9	GTBX	AFUc18408	3.	3.1E-33
25344 ENU09139 ANI61C1095 5:7772889	9	GTBX	AFUc13607	3.	5.8E-159
25345 ENU09140 ANI61C2891: 102356	9	GTBX	AFUc07028	4	4.3E-80
25346 ENU09141 ANI61C1096 4:141231	9	GTBX	"AFUc11060, AFUc15343"	£".	"3.8e-59, 5.7e-32"
25347 ENU09142 ANI61C1097 0:2035312	9	GTBX	"AFUc12156, AFUc15465, AFUc15465, FGR-00470"	4. 1. 2. 2.	"4.9e-55, 1.5e-10, 2.5e-45, 5.6e-11"
25348 ENU09143 ANI61C1097 4:24823605	9	GTBX	AFUc13816	. <del>4</del>	4.3E-55
25349 ENU09144 ANI61C1097 4:938110970	9	GTBX	CALc05781	1	1.6E-108
25350 ENU09145 ANI61C1097 5:8271721	9	GTBX	AFUc16580	9	6.4E-29
25351 ENU09146 ANI61C1097 5:77638178	0	GTBX	FGRc01084	9	6.3E-41
25352 ENU09147 ANI61C1097 8:1139422	O	GTBX	AFUc10468	18	8E-37

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ition															
% % id cvrg Description															
% id cvrg															
Blast Prob % "1.6e-66, 2.6e-15"	"7.9e-38, 2.7e-18"	2.2E-28	2.4E-33	4.4E-39	1.5E-33	"3.7e-48, 4.2e-14, 4.0e-19"	4.05-19	"6.6e- 111,	7.7e-89, 6.1e-	135"	2.1e-49	"2.4e-45, 3.0e-56"	1.6E-28	6.7E-26	"8.0e- 103, 1.6e-37, 5.1e-62"
Blast Score	,	• •	• •												
aat Score															
ıcbi gi															
Database Hit ncbi gi "AFUc10685, AFUc15487"	01566, 2071"	4598	8664	2150	3330	00802, .0080, .6223"	0273	07003, 17003,	0141"		4	"AFUc12472, AFUc14082"	1400	5756	"AFUc11534, AFUc18844, CALc03970"
	"AFUc01566, AFUc02071"	AFUc04598	AFUc08664	AFUc12150	AFUc13330	"AFUc00802 AFUc20080, CALC06223"		"AFUc07003, AFUc07003,	AFUc10141"		U00094	"AFUc12472 AFUc14082"	FGRc21400	AFUc15756	"AFUc11534 AFUc18844, CALc03970"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX		GTBX			GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos															
Primer 5 pos															
Contig source ANI61C9302: 1377310	25354 ENU09149 ANI61C9308: 30853645	ANI61C1098 0:35700	ANI61C1098 1:73547898	ANI61C1098 9:720515	ANI61C9317: 662250	ANI61C9317: 11092233		25360 ENU09155 ANI61C9318: 47465269			ANI61C1099 1:621883	ANI61C1099 7:82039278	25363 ENU09158 ANI61C1099 9:48955915	25364 ENU09159 ANI61C9322: 4841044	25365 ENU09160 ANI61C9325: 1369280
Seq num Seq id 25353 ENU09148	ENU09149	25355 ENU09150 ANI61C1 0:35700	25356 ENU09151 ANI61C1 1:73547	25357 ENU09152 ANI61C1 9:72051	25358 ENU09153	25359 ENU09154 ANI61C9 1109223		ENU09155			25361 ENU09156 ANI61C1 1:62188	25362 ENU09157	ENU09158	ENU09159	ENU09160
Seq num ( 25353 1	25354	25355	25356	25357	25358	25359		25360			25361	25362	25363	25364	25365

Seq num Seq id Contig source 5 25366 ENU09161 ANI61C8601: 28217	Primer Primer 5 pos 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc08235	aat Blast Blast Score Score Prob 4.1E-30	% % id cvrg Description
25367 ENU09162 ANI61C9331: 1071388		GTBX	AFUc13604	2.3E-35	
25368 ENU09163 ANI61C9332: 4445		GTBX	"AFUc10065, FGRc19031"	"1.5e-30, 2.9e-12"	
25369 ENU09164 ANI61C8605: 420208		GTBX	AFUc06416	5.3E-44	
25370 ENU09165 ANI61C9338: 292337		GTBX	"AFUc09246, AFUc11804, CALc06165, FGRc18522"	"3.8e-35, 2.2e- 225, 2.0e- 183,	
25371 ENU09166 ANI61C8612: 16372		GTBX	AFUc09632	0.1e-37 1.1E-45	
25372 ENU09167 ANI61C8612: 2351879		GTBX	"AFUc06058, AFUc09335"	"7.6e-07, 3.0e-80"	
25373 ENU09168 ANI61C9342: 27132181		GTBX	AFUc08063	5.5E-104	4
25374 ENU09169 ANI61C8614: 298115		GTBX	"AFUc15297, FGRc05338, FGR.25875"	"3.0e-73. 7.9e-24,	•
25375 ENU09170 ANI61C9344: 43794882		GTBX	AFUc11946	4.1E-23	
25376 ENU09171 ANI61C8619: 37982506		GTBX	AFUc12001	8.5E-46	
25377 ENU09172 ANI61C8620: 1357303		GTBX	"AFUc12034, CALc05986"	"2.6e-24, 3.2e-86"	
25378 ENU09173 ANI61C8620: 57946098		GTBX	AFUc14066	1.3E-110	0

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aat Blast Blast % Score Score Prob % id cvrg Description 9.2E-108	2.8E-77	2.2E-49	"7.5e-39, 2.4e-73, 1.6e-11"	7.7E-45	"1.2e- 107, 1.3e-33, 1.3e-37, 2.5e-81"	IE-31	"3.0e-11, 2.2e-37"	1.3E-25	5.8E-50	4.8E-31	1.6E-27	1.4E-28
Database Hit ncbi gi AFUc15687	AFUc06137	AFUc09529	"AFUc08848, AFUc09907, AFIIc20452"	AFUc19468	"AFUc08405, AFUc16754, FGRc14352, Z71257"	AFUc22414	"AFUc01391, FGRc18380"	AFUc10092	AFUc12786	AFUc11981	AFUc01678	AFUc14675
ner Selection is Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer Contig source 5 pos 3 pos 4 ANI61C9355:	5 ANI61C8628: 36656	6 ANI61C9357: 1371530	7 ANI61C7900: 25324277	8 ANI61C8631: 11032171	9 ANI61C8631: 41112590	0 ANI61C9363: 27583087	1 ANI61C8636: 895300	2 ANI61C8638: 1064405	3 ANI61C9371: 1504552	4 ANI61C8645: 11241467	5 ANI61C7918: 30111	6 ANI61C7918: 11041421
Seq num Seq id Contig source 25379 ENU09174 ANI61C9355: 1253680	25380 ENU09175 ANI61C8628: 36656	25381 ENU09176 ANI61C9357: 1371530	25382 ENU09177 ANI61C7900: 25324277	25383 ENU09178 ANI61C8631: 1103.2171	25384 ENU09179 ANI61C8631: 41112590	25385 ENU09180 ANI61C9363: 27583087	25386 ENU09181 ANI61C8636: 895300	25387 ENU09182 ANI61C8638: 1064405	25388 ENU09183 ANI61C9371: 1504552	25389 ENU09184 ANI61C8645: 11241467	25390 ENU09185 ANI61C7918: 30111	25391 ENU09186 ANI61.

Seq num Seq id Contig source 5 25392 ENU09187 ANI61C9377: 493810	Primer 5	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc12614, FGRc18368"	aat Blast Blast Score Score Prob "1.5e-	Blast % Prob % id cvrg Description "1.5e- 113,	Ę
25393 ENU09188 ANI61C9378: 9061421			GTBX	AFUc11838	2.00 1.51	2.0e-07 1.5E-77	
25394 ENU09189 ANI61C8650: 35123901			GTBX	AFUc12134	2.51	2.5E-43	
25395 ENU09190 ANI61C7924: 4128			GTBX	AFUc15732	2.7]	2.7E-26	
25396 ENU09191 ANI61C8653: 1726828			GTBX	AFUc13073	1.2]	1.2E-130	
25397 ENU09192 ANI61C9383: 65307124			GTBX	AFUc17773	5.3]	5.3E-67	
25398 ENU09193 ANI61C8656: 38513351			GTBX	AFUc05544	8.9]	8.9E-73	
25399 ENU09194 ANI61C8657: 133693			GTBX	AFUc08713	1.91	1.9E-58	
25400 ENU09195 ANI61C8659: 24963023			GTBX	"AFUc03782, FGRc10049"	1.0	"1.0e-18, 4.9e-38"	
25401 ENU09196 ANI61C7930: 6591267			GTBX	"AFUc05717, AFUc21348"	"6.6 1.6	"6.6e-43, 1.6e-09"	
25402 ENU09197 ANI61C8661: 33133669			GTBX	FGRc07994	1.6	I.6E-28	
25403 ENU09198 ANI61C8667: 78575			GTBX	AFUc05732	5.1)	5.1E-32	
25404 ENU09199 ANI61C9398: 39177			GTBX	AFUc20294	1.1	1.1E-23	
25405 ENU09200 ANI61C7941: 92325			GTBX	CALc05278	1.2]	1.2E-32	

aat Blast Blast %  Score Score Prob % id cvrg Description "1.0e-15, 4.4e-33"	"1.1e-42, 2.9e-13, 1.3e-27"	"8.2e-37, 7.6e-63"	5.6E-37	1.5E-32	"5.6e-34, 1.9e-46"	"6.3e-98, 1.0e-48"	1.7E-30	"1.7e-30, 5.7e- 110"	4.8E-39	4.4E-51	9.1E-56
Database Hit ncbi gi "FGRc08201, Y13135"	"AFUc00793, FGRc05104, FGRc16937"	"AFUc21738" AFUc21738"	AFUc05878	AFUc14227	"AFUc18036, FGRc00673"	"AFUc08873, FGRc22249"	AFUc18580	"AFUc02640, Y13134"	FGRc17279	AFUc11561	AFUc08840
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos											
Primer 6 5 pos ):	::	ë	↔	9:	7:	<del>.;</del>	.; <u>.</u>	<b>::</b>	÷.	ö	.;
Seq num Seq id Contig source 25406 ENU09201 ANI61C8670: 1370185	25407 ENU09202 ANI61C8675: 1001198	25408 ENU09203 ANI61C7953: 1094460	25409 ENU09204 ANI61C8684: 64989	25410 ENU09205 ANI61C8686: 43155067	25411 ENU09206 ANI61C8687: 20021217	25412 ENU09207 ANI61C8694: 1591479	25413 ENU09208 ANI61C7976: 32271	25414 ENU09209 ANI61C5001: 14031140	25415 ENU09210 ANI61C5009: 24377	25416 ENU09211 ANI61C7980: 531288	25417 ENU09212 ANI61C5019. 76693
Seq num Sec 25406 EN	25407 EN	25408 EN	25409 EN	25410 EN	25411 EN	25412 EN	25413 EN	25414 EN	25415 EN	25416 EN	25417 EN

# odina ce

aat Blast Blast % Score Score Prob % id cvrg Description "1.9e-44, 1.1e- 118, 1.5e- 129, 2.7e-65, 7.2e-77"	"5.0e-68, 1.7e-70"	9.3E-47	3.8E-70	"3.5e-27, 5.0e-08"	"1.9e-46, 2.0e-41, 3.3e-09"	6.6E-33	4.4E-144	6.6E-29	1.8E-48	2.4E-249	4.4E-34	2.2E-39
Selection Basis Database Hit ncbi gi GTBX "AFUc01564, AFUc09051, AFUc11907, AFUc11907"	GTBX "AFUc08580, CALc03532"	GTBX AFUc03796	GTBX AFUc06232	GTBX "AFUc14677, AFUc15942"	GTBX "AFUc03507, AFUc09984, AFIIc12002"	GTBX AFUc15029	GTBX AFUc13413	GTBX AFUc14056	GTBX AFUc13039	GTBX AFUc12578	GTBX AFUc13345	GTBX AFUc12517
Seq  Primer Primer Sel  num Seq id Contig source 5 pos 3 pos Ba  25418 ENU09213 ANI61C7995:  16016527	25419 ENU09214 ANI61C4300: GT 16961159	25420 ENU09215 ANI61C4303: GT 8436	25421 ENU09216 ANI61C5033: GT 401000	25422 ENU09217 ANI61C5036: GT 600238	25423 ENU09218 ANI61C4307: G7 1506298	25424 ENU09219 ANI61C5037: GT 994581	25425 ENU09220 ANIGIC4310: GT 1263517	25426 ENU09221 ANI61C4314: GT 115406	25427 ENU09222 ANI61C4317: G7 1103288	25428 ENU09223 ANI61C4320: G7 6162524	25429 ENU09224 ANI61S957:5 G7 401	25430 ENU09225 ANI61C3603: G7 5547

# 

Blast Blast % Score Prob % id cvrg Description 1.4E-40	"3.8e-48, 1.2e-40"	"1.7e-54, 1.7e-61"	3.4E-35	"2.4e-17, 1.1e-94"	3.2E-33	6.9E-65	"3.9e-58, 1.8e-10"	3.4E-44	4.9E-24	"6.4e-96, 5.4e- 119"	"2.3e- 108, 1.2e-	"2.0e-37, 1.8e-12"	"5.6e-33, 4.7e-38, 2.4e-29"
5													
Database Hit ncbi gi AFUc15803	"AFUc13626, FGRc03674"	"AFUc13451, AFUc13451"	AFUc01317	"AFUc12501, CALc06236"	AFUc11581	AFUc07024	"AFUc12259, Y13138"	CALc03177	FGRc06045	"AFUc13163, AFUc13851"	"AFUc11103, D50617"	"AFUc03814, AFUc21290"	"AFUc13706, AFUc22334, FGRc07656"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 25431 ENU09226 ANI61C4336: 7281	25432 ENU09227 ANI61C4337: 952483	25433 ENU09228 ANI61C4338: 66696	25434 ENU09229 ANI61C4341: 829287	25435 ENU09230 ANI61C4344: 30491141	25436 ENU09231 ANI61C3616: 12161622	25437 ENU09232 ANI61C3617: 1144657	25438 ENU09233 ANI61C3619: 75548	25439 ENU09234 ANI61C3621: 68522	25440 ENU09235 ANI61C3624: 887140	25441 ENU09236 ANI61C3626: 9053359	25442 ENU09237 ANI61C5085: 19155	25443 ENU09238 ANI61C3627: 76368229	25444 ENU09239 ANI61C4357: 33584103

# outen contain

aat Blast Blast % Score Score Prob % id cvrg Description 2.3E-91	1.4E-42	1.8E-48	8E-41	1.6E-24	2.5E-29	1.1E-108	1.2E-24	"7.5e-43, 3.5e-19"	3.1E-153	"3.6e-42, 8.1e-24, 5.2e- 105, 8.5e-21"	9E-43	9.6E-53
Selection Basis Database Hit ncbi gi GTBX AFUc09818	GTBX AFUc08911	GTBX AFUc00666	GTBX AFUc15350	GTBX AFUc20583	GTBX AFUc10569	GTBX AFUc11858	GTBX AFUc05222	GTBX "AFUC18364, CALc04995"	GTBX AFUc15969	GTBX "AFUc13516, AFUc14043, AFUc15051, FGRc01953"	GTBX AFUc10688	GTBX AFUc09914
Seq Primer Primer Se num Seq id Contig source 5 pos 3 pos Ba 25445 ENU09240 ANI61C4358: G711564	25446 ENU09241 ANI61C4359: G7 1631020	25447 ENU09242 ANI61C5089: G7 65538	25448 ENU09243 ANI61S4199: G7 93693	25449 ENU09244 ANI61C3636: G <sup>*</sup> 64477685	25450 ENU09245 ANI61C4365: G' 67429	25451 ENU09246 ANI61C4368: G <sup>°</sup> 27091873	25452 ENU09247 ANI61C5097: G' 48744	25453 ENU09248 ANI61S3472: G	25454 ENU09249 ANI61C3640: G' 1580893	25455 ENU09250 ANI61C4370: G'	25456 ENU09251 ANI61C2912: G 62916	25457 ENU09252 ANI61C4373: G 445695

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25458 ENU09253 ANI61C3645: 53206232	Selection Basis GTBX	Database Hit ncbi gi FGRc09513	aat Blast Blast Score Score Prob % id 1.3E-21	% id cvrg Description
25459 ENU09254 ANI61C4378: 2391305	GTBX	"AFUc02594, AFUc07825"	"2.6e-23, 4.9e-61"	
25460 ENU09255 ANI61S3489: 113.452	GTBX	CALc04906	9.1E-48	
25461 ENU09256 ANI61C2920: 9651437	GTBX	Y13140	2.1e-24	
25462 ENU09257 ANI61C3650: 18163768	GTBX	AFUc15925	1.7E-151	
25463 ENU09258 ANI61C4382: 39667	GTBX	AFUc06115	3.9E-28	
25464 ENU09259 ANI61C3655: 5607	GTBX	"AFUc04082, FGRc03487"	"1.1e-16, 2.7e-26"	
25465 ENU09260 ANI61C2927: 556.311	GTBX	AFUc10442	7.5E-25	
25466 ENU09261 ANI61C2932: 377873	GTBX	CALc04475	4.6E-79	
25467 ENU09262 ANI61C3661: 6132	GTBX	"AFUc01462, AFUc19592"	"1.1e-31, 2.0e-18"	
25468 ENU09263 ANI61C4391: 2513355	GTBX	"AFUc13024, AFUc15301"	"2.3e-68, 7.6e- 132"	
25469 ENU09264 ANIGIC4391: 5770.4632	GTBX	"AFUc08279, Y13139"	"1.2e-32, 5.3e-65"	
25470 ENU09265 ANI61C2934: 3351188	GTBX	"AFUc11881, AFUc11881"	"1.7e-77, 2.7e-77"	
25471 ENU09266 ANI61C4392: 91857	GTBX	AFUc07215	1.1E-54	

# rocette centro

Seq num Seq id Contig source 25472 ENU09267 ANI61C4393: 4780	Contig source ANI61C4393: 4780	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc13630, Y13134"	aat Blast Score Score	Blast Prob "4.6e-34, 2.5e-61"	% id cvrg Description
3 ENU09268	ANI61C3663: 74413			GIBA	Aruci 2330, CALc05628, FGRc10684"		8.46-43, 2.3e-41, 1.2e-68"	
25474 ENU09269 ANI61C2936: 3788	ANI61C2936: 3788			GTBX	"AFUc11814, FGRc11194"		"6.4e-45, 1.3e-77"	
25475 ENU09270 ANI61C3669: 6744	ANI61C3669: 6744			GTBX	CALc05387		6.1E-60	
25476 ENU09271 ANI61C4398: 167484	ANI61C4398: 167484			GTBX	AFUc05879		4.1E-42	
25477 ENU09272 ANI61C2942: 5991304	ANI61C2942: 5991304			GTBX	"AFUc06459, AFUc13777"		"3.1e-14, 1.9e-50"	
8 ENU09273	25478 ENU09273 ANI61C3681: 8201754			GTBX	"AFUc14966, CALc04781"		"6.1e- 140, 9.4e-56"	
25479 ENU09274 ANI61C3692: 64971	ANI61C3692: 64971			GTBX	"AFUc02774, AFUc02886"		"1.3e-41, 1.0e-06"	
0 ENU09275	25480 ENU09275 ANI61C3696: 4633			GTBX	AFUc12839		7.9E-64	
11 ENU09276	25481 ENU09276 ANI61C2969: 36382636			GTBX	"AFUc09259, AFUc09259"		"2.0e-40, 5.6e-58"	
2 ENU09277	25482 ENU09277 ANI61C2971: 73501			GTBX	FGRc24981		1.9E-21	
3 ENU09278	25483 ENU09278 ANI61C2976: 1318175			GTBX	AFUc04211		5.4E-93	
4 ENU09279	25484 ENU09279 ANI61C2999: 8761			GTBX	Z71256		6.5e-84	
5 ENU09280	25485 ENU09280 ANI61C9402: 2171856			GTBX	"FGRc03487, FGRc09159, FGRc09159, FGRc23883"		"1.3e-37, 4.4e-29, 8.6e-30, 5.8e-11"	

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Seq num Seq id 25486 ENU09281	Contig source ANI61C9439: 80469	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc15622	aat Blast Score Score	Blast Prob 8.9E-30	% id cvrg Description
25487 ENU09282 ANI61C9440: 779462	ANI61C9440: 779462			GTBX	AFUc11219		3.3E-61	
25488 ENU09283 ANI61C9440: 34733216	ANI61C9440: 34733216			GTBX	AFUc08291		8.7E-44	
25489 ENU09284 ANI61C9441: 564293	ANI61C9441: 564293			GTBX	AFUc08255		8.9E-26	
25490 ENU09285 ANI61C8713: 857341	ANI61C8713: 857341			GTBX	AFUc05686		3.6E-29	
25491 ENU09286 ANI61C8714: 13471968	ANI61C8714: 13471968			GTBX	AFUc20415		2E-24	
25492 ENU09287 ANI61C9445: 2561691	ANI61C9445: 2561691			GTBX	AFUc07629		5.2E-69	
25493 ENU09288 ANI61C9446: 221547	ANI61C9446: 221547			GTBX	AFUc12171		4.8E-35	
25494 ENU09289 ANI61C9451: 49055724	ANI61C9451: 49055724			GTBX	"AFUc05775, CALc05482"		"7.3e-64, 9.1e-41"	
25495 ENU09290 ANI61C 765153	ANI61C8722: 765153			GTBX	AFUc03370		5.4E-35	
25496 ENU09291 ANI61C8722: 26063753	ANI61C8722: 26063753			GTBX	"AFUc03885, AFUc11035"		"1.8e-30, 3.8e-53"	
25497 ENU09292 ANI61C 48079	ANI61C9455: 48079			GTBX	AFUc18390		2.9E-23	
25498 ENU09293 ANI61C9456: 1440613	ANI61C9456: 1440613			GTBX	AFUc12641		1.1E-86	
25499 ENU09294 ANI61C8727: 41833316	ANI61C8727: 41833316			GTBX	AFUc09501		1.1E-72	

# corcato carand

Seq num Seq id 25500 ENU09295	Contig source ANI61C9459: 7591691	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc18002, AFUc20595"	aat Blast Score Score	Blast Prob "3.4e-58, 1.5e-39"	% id cvrg Description	
25501 ENU09296 ANI61C8730: 43975083	ANI61C8730: 43975083			GTBX	"AFUc07855, FGRc11749"		"1.1e-24, 1.7e-09"		
25502 ENU09297 ANI61C9461: 19972263	ANI61C9461: 19972263			GTBX	AFUc03878		2.7E-36		
25503 ENU09298 ANI61C9464: 10191336	ANI61C9464: 10191336			GTBX	AFUc10300		2.6E-29		
25504 ENU09299 ANI61C9465: 28843407	ANI61C9465: 28843407			GTBX	"AFUc08665, AFUc08665"		"8.6e- 122, 9.5e-97"		
25505 ENU09300 ANI61C8737: 1091741	ANI61C8737: 1091741			GTBX	AFUc12153		2.4E-35		
25506 ENU09301 ANI61C9469: 2481142	ANI61C9469: 2481142			GTBX	AFUc11644		8.5E-33		
25507 ENU09302 ANI61C8741: 8561840	ANI61C8741: 8561840			GTBX	AFUc13104		1.4E-61		
25508 ENU09303 ANI61C9470: 774202	ANI61C9470: 774202			GTBX	AFUc15952		4.4E-72		
25509 ENU09304 ANI61C8743: 40324467	ANI61C8743: 40324467			GTBX	AFUc15883		8.5E-24		
25510 ENU09305 ANI61C8745: 77811	ANI61C8745: 77811			GTBX	AFUc07060		4E-35		
25511 ENU09306 ANIGLC9477: 29623512	ANI61C9477: 29623512			GTBX	AFUc09065		2E-58		
25512 ENU09307 ANI61C9479: 12307	ANI61C9479: 12307			GTBX	AFUc14503		1.5E-32		
25513 ENU09308 ANI61C8750: 1390.2176	ANI61C8750: 13902176			GTBX	CALc06230		1.2E-262		

### ngungen need

Seq num Seq id 25514 ENU09309	Contig source ANI61C8751: 240414	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc04130, AFUc16265"	aat Blast Score Score	Blast Prob "1.5e-29, 8.4e-27"	% id cvrg Description	ription
25515 ENU09310 ANI61C8757: 16401332	ANI61C8757: 16401332			GTBX	AFUc08891		7.1E-22		
25516 ENU09311 ANI61C8759: 31323793	ANI61C8759: 31323793			GTBX	FGRc16689		7.5E-21		
25517 ENU09312 ANI61C9491: 26151865	ANI61C9491: 26151865			GTBX	CALc06160		8E-24		
25518 ENU09313 ANI61C8765: 548896	ANI61C8765: 548896			GTBX	AFUc09309		1.1E-36		
25519 ENU09314 ANI61C8767: 18691250	ANI61C8767: 18691250			GTBX	AFUc14377		4.9E-28		
25520 ENU09315 ANI61C9497: 10701664	ANI61C9497: 10701664			GTBX	"AFUc10902, AFUc10902"		"8.1e-43, 9.7e-22"		
25521 ENU09316 ANI61C8780: 12542080	ANI61C8780: 12542080			GTBX	"AFUc15659, FGRc19707"		"1.3e-15, 1.2e-29"		
25522 ENU09317 ANI61C8781: 19831047	ANI61C8781: 19831047			GTBX	"AFUc03553, AFUc07731"		"1.7e- 119, 2 6e-30"		
25523 ENU09318 ANI61C8795: 1064834	ANI61C8795: 1064834			GTBX	FGRc02905		2.8E-39		
25524 ENU09319 ANI61C8797: 620834	ANI61C8797: 620834			GTBX	AFUc13831		3.4E-59		
25525 ENU09320 ANI61C8797: 14672151	ANI61C8797: 14672151			GTBX	"AFUc03642, AFUc13831"		"2.8e-13, 3.4e-59"		
25526 ENU09321 ANI61C5102: 300535	ANT61C5102: 300535			GTBX	AFUc19728		2.1E-22		
25527 ENU09322 ANI61C5103: 4021	ANI61C5103: 4021			GTBX	AFUc14207		9.4E-86		

Seq num Seq id Contig source 5 25528 ENU09323 ANI61C5110: 1141410	Primer 15 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc18303, CALc06183"	aat Blast Score Score	Blast Prob "1.2e-34, 1.4e-90"	% id cvrg Description	
25529 ENU09324 ANI61C5111: 9121773			GTBX	"AFUc05704, AFUc13358"		"1.1e-34, 1.1e-34"		
25530 ENU09325 ANI61C5115: 13451022			GTBX	AFUc19450		1.1E-44		
25531 ENU09326 ANI61C5119: 58214			GTBX	AFUc07458		2.7E-28		
25532 ENU09327 ANI61C5124: 8041031			GTBX	AFUc07545		5.5E-22		
25533 ENU09328 ANI61C4400: 23061797			GTBX	"FGRc08787, FGRc14740"		"7.0e-21, 4.4e-17"		
25534 ENU09329 ANI61C4401: 23451654			GTBX	"AFUc05876, FGRc05155"		"4.8e-30, 7.0e-10"		
25535 ENU09330 ANI61C4406: 538.251			GTBX	AFUc07366		1.4E-21		
25536 ENU09331 ANI61C4407: 41545342			GTBX	"AFUc01633, AFUc19340"		"6.1e-20, 1.6e-39"		
25537 ENU09332 ANI61C4408: 13903			GTBX	AFUc13334		8E-99		
25538 ENU09333 ANI61C5137: 103413			GTBX	U00091		3.4e-45		
25539 ENU09334 ANI61C4409: 5792167			GTBX	"AFUc02131, CALc04637, FGB_10200"		"1.1e-80, 4.6e-17, 7.3e-65"		
25540 ENU09335 ANI61S4243: 78437			GTBX	Y18138		2.5e-15		
25541 ENU09336 ANI61S3519: 56256			GTBX	AFUc13413		4E-24		

Seq Primer num Seq id Contig source 5 pos 25542 ENU09337 ANI61C5143: 665148	Primer Primer 5 pos 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc22527	aat Blast Blast Score Score Prob 2.5E-69	% id cvrg Description
25543 ENU09338 ANI61C4415: 697308		GTBX	AFUc08588	8.1E-50	
25544 ENU09339 ANI61C4415: 19442984		GTBX	"AFUc14631, Z71256"	"5.7e- 117, 4.2e-40"	
25545 ENU09340 ANI61C5153: 4001153		GTBX	AFUc15665	9.9E-110	
25546 ENU09341 ANI61C4428: 2186509		GTBX	"AFUc03693, AFUc15500"	"1.3e-09, 4.9e-36"	
25547 ENU09342 ANI61C4429: 456989		GTBX	AFUc02454	1.9E-48	
25548 ENU09343 ANI61C4430: 5906		GTBX	"AFUc0 <i>5777</i> , AFUc11518"	"3.2e-11, 3.9e-35"	
25549 ENU09344 ANI61C4431: 8651682		GTBX	CALc05985	7.5E-34	
25550 ENU09345 ANI61C4431: 22881929		GTBX	AFUc19720	1.9E-32	
25551 ENU09346 ANI61C5161: 64798758		GTBX	"AFUc15497, FGRc01538"	"2.1e- 195, 1.2e-29"	
25552 ENU09347 ANI61C4435: 44619		GTBX	AFUc10109	2.3E-49	
25553 ENU09348 ANI61C4436: 5625		GTBX	"AFUc20304, FGRc08260"	"2.3e-42, 1.2e-10"	
25554 ENU09349 ANI61C4439: 603957		GTBX	"AFUc15143, AFUc22336"	"4.2e-45, 1.0e-09"	
25555 ENU09350 ANIGIC3716: 49552		GTBX	AFUc17201	8.4E-27	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25556 ENU09351 ANI61C5184:	Selection Basis GTBX	Database Hit ncbi gi FGRc06929	aat Blast Blast % Score Score Prob % id cvrg 2.5E-27	Description
25557 ENU09352 ANI61C5184: 19582668	GTBX	"AFUc02805, AFUc21089"	"2.8e-37, 4.9e-21"	
25558 ENU09353 ANI61C5189: 101877	GTBX	AFUc11900	1.1E-105	
25559 ENU09354 ANI61C3732: 61673	GTBX	AFUc01401	2.1E-67	
25560 ENU09355 ANI61C3733: 32101934	GTBX	"FGRc03487, FGRc09159"	"5.7e-40, 2.8e-32"	
25561 ENU09356 ANI61C5191: 8424	GTBX	AFUc09001	5.6E-37	
25562 ENU09357 ANI61C3738: 6715	GTBX	"AFUc03774, AFUc13364"	"8.2e-10, 1.8e-39"	
25563 ENU09358 ANI61C5199: 15781127	GTBX	AFUc14538	3.3E-24	
25564 ENU09359 ANIGIS2843: 42810	GTBX	"AFUc14444, FGRc10441"	"8.6e-31, 9.2e-07"	
25565 ENU09360 ANI61C3747: 51467	GTBX	AFUc14515	1.4E-45	
25566 ENU09361 ANI61S3584: 97486	GTBX	AFUc10638	2.5E-31	
25567 ENU09362 ANI61C3751: 892219	GTBX	FGRc00730	4.1E-26	
25568 ENU09363 ANI61C3754: 43874890	GTBX	"AFUc02406, CALc04204"	"8.0e-11, 5.7e-83"	
25569 ENU09364 ANI61C4484: 195646	GTBX	AFUc11050	2.8E-26	

# ngungan nagag

aat Blast Blast % Score Score Prob % id cvrg Description 2.8E-121	1E-32	2E-55	6.8E-93	4E-67	2.5E-74	"1.3e-28, 3.1e-25"	"3.1e- 107, 8.7e-28"	4.3E-84	6E-62	8.8E-24	"1.3e-22, 3.5e-14"	"5.7e-54, 1.2e-07"	"1.8e-65, 7.3e- 119"
on Database Hit ncbi gi AFUc11852	FGRc26076	AFUc00783	AFUc01513	FGRc10958	AFUc15397	"AFUc21795, FGRc13545"	"AFUc09448, FGRc15416"	. AFUc15598	. AFUc15752	. FGRc08493	. "AFUc02590, AFUc21220"	"AFUc02035, FGRc16341"	. "AFUc08207, AFUc09870"
ler Selection s Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos :					2.	<u>.</u> .	.:	\ <del>.</del>	<u></u>	150	÷	ت	÷
Seq num Seq id Contig source 25570 ENU09365 ANI61C4485: 4701338	25571 ENU09366 ANI61C3758: 368568	25572 ENU09367 ANI61S2863: 456103	25573 ENU09368 ANI61C4495: 836438	25574 ENU09369 ANI61C4496: 9731308	25575 ENU09370 ANI61C4497: 1059277	25576 ENU09371 ANI61C3777: 414651	25577 ENU09372 ANI61C3785: 107087	25578 ENU09373 ANI61C3786: 347670	25579 ENU09374 ANI61C9504: 1509983	25580 ENU09375 ANI61C9505: 6593	25581 ENU09376 ANIGIC9508: 1395319	25582 ENU09377 ANIGLC9521: 1526810	25583 ENU09378 ANI61C9523: 219413

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Seq num Seq id Contig source 25584 ENU09379 ANI61C9524: 491986		Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc15203	aat Blast Score Score	Blast Prob 2.5E-28	% id cvrg Description
25585 ENU09380 ANI61C9528: 1204737	ANI61C9528: 1204737			GTBX	AFUc05005		1.1E-24	
25586 ENU09381 ANI61 36893	ANI61C9529: 36893			GTBX	AFUc05865		5.5E-26	
25587 ENU09382 ANI61C9531: 7242	ANI61C9531: 7242			GTBX	AFUc08448		6.3E-38	
25588 ENU09383 ANI61C8803: 601376	ANI61C8803: 601376			GTBX	"AFUc06649, AFUc09276, AFUc09645, AFUc15313,		"8.5e-10, 8.2e-10, 6.1e-38, 3.1e-53,	
25589 ENU09384 ANI61C8808: 34124903	ANI61C8808: 34124903			GTBX	FGRc04144		3.2e-08 2.6E-64	
25590 ENU09385 ANI61C8809: 3041298	ANI61C8809: 3041298			GTBX	"AFUc10278, FGRc24365"		"1.3e-76, 1.7e-38"	
25591 ENU09386 ANI61C9539: 14841182	ANI61C9539: 14841182			GTBX	AFUc03644		3.4E-48	
25592 ENU09387 ANI61C8814: 38675544	ANI61C8814: 38675544			GTBX	AFUc12826		4.6E-78	
25593 ENU09388 ANI61C9543: 28687	ANI61C9543: 28687			GTBX	"AFUc05060, AFUc19153"		"5.8e-10, 7.8e-22"	
25594 ENU09389 ANI61C8815: 226648	ANI61C8815: 226648			GTBX	AFUc22266		2.3E-27	
25595 ENU09390 ANI61C8818: 18721054	ANI61C8818: 18721054			GTBX	AFUc13384		9.4E-45	
25596 ENU09391 ANI61C9547: 55656	ANI61C9547: 55656			GTBX	AFUc09688		6.5E-47	

Seq num Seq id 25597 ENU09392	Contig source ANI61C9548: 1206482	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc02615	aat Blast B Score Score P 5	Blast Prob 5E-21	% id cvrg Description
25598 ENU09393 ANI61C9549: 160864	ANI61C9549: 160864			GTBX	AFUc01363	2	2.1E-25	
25599 ENU09394 ANI61C8820: 236749	ANI61C8820: 236749			GTBX	"AFUc00774, AFUc02877, AFUc05794, AFUc15944,	: 1000	"8.7e-55, 1.1e-11, 3.2e-60, 6.1e-25,	
25600 ENU09395 ANI61C8821: 1333384	ANI61C8821: 1333384			GTBX	AFUc10083	) <b>C</b>	7.2E-44	
25601 ENU09396 ANI61C8821: 16192665	ANI61C8821: 16192665			GTBX	"FGRc04178, Z71256"	: 0	"5.1e-08, 6.6e-88"	
25602 ENU09397 ANI61C9553: 2145406	ANI61C9553: 2145406			GTBX	"AFUc06513, AFUc07337, CAL c06139"	: 0/4	"1.2e-55, 9.6e-62, 4.0e-40"	
25603 ENU09398 ANI61C9556: 73137830	ANI61C9556: 73137830			GTBX	FGRc11417	. 2	2.8E-61	
25604 ENU09399 ANI61C8827: 1639428	ANI61C8827: 1639428			GTBX	FGRc06586		7.5E-35	
25605 ENU09400 ANI61C8831: 22992823	ANI61C8831: 22992823			GTBX	"AFUc01894, CALc05378"	: -	"4.2e-36, 1.8e-38"	
25606 ENU09401 ANI61C9566: 23821796	ANI61C9566: 23821796			GTBX	"AFUc14024, FGRc03629"	Ξ <b>V</b> )	"8.2e-20, 5.8e-27"	
25607 ENU09402 ANI61C9567: 17212586	ANI61C9567: 17212586			GTBX	AFUc08775	~	2.6E-28	
25608 ENU09403 ANI61C9569: 1936900	ANI61C9569: 1936900			GTBX	"AFUc11045, FGRc07076"	- (4	"1.3e-26, 2.2e-09"	
25609 ENU09404 ANI61C9572: 30192194	ANI61C9572: 30192194			GTBX	CALc05999	7	4.9E-122	

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Seq num Seq id Contig source 25610 ENU09405 ANI61C8846: 2490	Contig source ANI61C8846: 2490	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc09502	aat Blast Bl Score Score Pr 2.	Blast % Prob % id cvrg Description 2.1E-50	
25611 ENU09406 ANI61C9579: 41503347	ANI61C9579: 41503347			GTBX	AFUc05155	.2	2.4E-30	
25612 ENU09407 ANI61C9582: 1668221	ANI61C9582: 1668221			GTBX	"AFUc09791, AFUc14294,		"1.2e-28, 3.4e-45, 5.5-78"	
25613 ENU09408 ANI61C8854: 6331820	ANI61C8854: 6331820			GTBX	AFUc08210" AFUc08210"	;	"1.4e-07, 1.2e-33"	
25614 ENU09409 ANI61C8857: 23342536	ANI61C8857: 23342536			GTBX	AFUc06435	1.	1.5E-121	
25615 ENU09410 ANI61C9592: 105520	ANI61C9592: 105520			GTBX	"FGRc09345, FGRc21977"	. i	"6.9e-29, 2.9e-14"	
25616 ENU09411 ANI61C9595: 1129674	ANI61C9595: 1129674			GTBX	AFUc14898	9	6.6E-58	
25617 ENU09412 ANI61C8867: 80326	ANI61C8867: 80326			GTBX	"AFUc08398, CALc05816"	¥' ⊷	"5.9e-24, 1.3e-17"	
25618 ENU09413 ANI61C8873: 81527032	ANI61C8873: 81527032			GTBX	AFUc12824	6	2.7E-89	
25619 ENU09414 ANI61C8875: 121277	ANI61C8875: 121277			GTBX	AFUc14483	4	4.9E-162	
25620 ENU09415 ANI61C8878: 44934	ANI61C8878: 44934			GTBX	AFUc14882	7.	7.3E-46	
25621 ENU09416 ANI61C8879: 14042768	ANI61C8879: 14042768			GTBX	AFUc14241	<b>-</b>	1.9E-70	
25622 ENU09417 ANI61C8884: 106753	ANI61C8884: 106753			GTBX	AFUc07086	4	4.5E-95	
25623 ENU09418 ANI61C8888: 11561536	ANI61C8888: 11561536			GTBX	U00093	<b>-</b>	1.2e-74	

				•			77	8	
Seq num Seq id 25624 ENU09419	Contig source ANI61C8889: 7021898	5 pos	3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc03016, CALc03652"	aat Biast Score Score	Prob "1.4e-55, 2.8e-59"	% id cvrg Description	
25625 ENU09420 ANI61C8892: 1683192	ANI61C8892: 1683192			GTBX	"AFUc13932, FGRc11747, FGRc17309, FGRc26009"		"1.4e-25, 1.3e-10, 5.3e-09, 1.1e-16"		
25626 ENU09421 ANI61C8895: 67904	ANI61C8895: 67904			GTBX	"AFUc11204, AFUc11814"		"2.5e-34, 1.2e- 104"		
25627 ENU09422 ANI61C5207: 316663	ANI61C5207: 316663			GTBX	AFUc15608		1.5E-46		
25628 ENU09423 ANI61C5207: 1872793	ANI61C5207: 1872793			GTBX	"AFUc03870, AFUc07633, AFUc19031"		"6.3e-16, 1.2e-19, 9.9e-70"		
25629 ENU09424 ANI61C5208: 25362216	ANI61C5208: 25362216			GTBX	"AFUc06181, Y13138"		"1.5e-32, 9.0e- 162"		
25630 ENU09425 ANI61C5209: 14572136	ANI61C5209: 14572136			GTBX	"AFUc17725, FGRc11373"		"3.9e-27, 7.4e-19"		
25631 ENU09426 ANI61C5210: 2139105	ANT61C5210: 2139105			GTBX	AFUc15196		3.7E-186		
25632 ENU09427 ANI61C5 2509276	ANI61C5215: 25092763			GTBX	AFUc15348		7.2E-121		
25633 ENU09428 ANI61C5222: 2322719	ANI61C5222: 2322719			GTBX	"AFUc07927, FGRc02874"		"7.9e-86, 9.0e-10"		
25634 ENU09429 ANI61C5 147213	ANI61C5224: 147213			GTBX	CALc05716		1.7E-119		
25635 ENU09430 ANI61C5 399962	) ANI61C5228: 399962			GTBX	AFUc14750		1.2E-90		
25636 ENU09431 ANI61S3608: 177573	ANI61S3608: 177573			GTBX	AFUc22203		1.8E-23		

Seq num Seq id Contig source 25637 ENU09432 ANI61C4506: 49929	Contig source ANI61C4506: 49929	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc15788	aat Blast Score Score	Blast Prob 9.6E-33	% % id cvrg Description	
25638 ENU09433 ANI61C5237: 4201271	ANI61C5237: 4201271			GTBX	AFUc14942		6.9E-104		
25639 ENU09434 ANIGIC5247: 41104852	ANI61C5247: 41104852			GTBX	AFUc13730		1E-97		
25640 ENU09435 ANI61C4519: 2052587	ANI61C4519: 2052587			GTBX	AFUc15419		5.4E-127		
25641 ENU09436 ANI61C5251: 67247	ANI61C5251: 67247			GTBX	Y13137		4.1e-43		
25642 ENU09437 ANI61C4526: 14131054	ANI61C4526: 14131054			GTBX	AFUc15744		1.3E-147		
25643 ENU09438 ANI61C5256: 67426	ANI61C5256: 67426			GTBX	"AFUc06812, AFUc08626"		"1.7e-44, 2.8e-09"		
25644 ENU09439 ANI61C4528: 509147	ANI61C4528: 509147			GTBX	AFUc15759		1.9E-29		
25645 ENU09440 ANI61S4368: 60639	ANI61S4368: 60639			GTBX	AFUc07754		2.2E-21		
25646 ENU09441 ANI61C3803: 10962	ANI61C3803: 10962			GTBX	"AFUc08591, AFUc13887"		"1.1e-55, 4.4e-75"		
25647 ENU09442 ANI61C3805: 40353580	ANI61C3805: 40353580			GTBX	AFUc04676		6.3E-45		
25648 ENU09443 ANI61C3808: 743.411	ANI61C3808: 743411			GTBX	Y13138		5.8e-14		
25649 ENU09444 ANI61C5269: 13942229	ANI61C5269: 13942229			GTBX	"AFUc02280, AFUc22008"		"9.4e-57, 2.0e-43"		
25650 ENU09445 ANI61C3810: 82437	ANI61C3810: 82437			GTBX	AFUc15201		4E-52		

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aat Blast Blast % Score Score Prob % id cvrg Description 3.5E-30	"1.7e-65, 4.7e-26"	"4.6e-26, 7.9e-35, 1.6e-43"	"5.4e-27, 1.6e-92"	2.7E-75	4.7E-56	3.2E-45	"1.2e-24, 2.7e-07"	7.4E-60	2.8E-21	"5.9e-40, 3.0e-16, 6.7e-17"	4.8E-36	"5.6e-24, 6.7e-29, 3.4e-13"	3.4E-31
on Database Hit ncbi gi AFUc06467	"AFUc02869, AFUc02869"	FGRc12841, FGRc22473,		AFUc12851	: AFUc15435	AFUc18864	. "AFUc04510, AFUc18595"	. AFUc12507	; FGRc23435	CALC02020, CALC02020, V13134"	·	( "AFUc12628, AFUc12628, ECD-07656"	
Primer Selection 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq Primer num Seq id Contig source 5 pos 25651 ENU09446 ANI61C3811: 13761654	25652 ENU09447 ANI61C4542: 916574	25653 ENU09448 ANI61C3813: 18463158	25654 ENU09449 ANI61C5273: 21156	25655 ENU09450 ANI61C3817: 781162	25656 ENU09451 ANI61C3821: 672411	25657 ENU09452 ANI61C4551: 151475	25658 ENU09453 ANI61C5280: 18402502	25659 ENU09454 ANI61C3823: 22252	25660 ENU09455 ANI61C3824: 595981	25661 ENU09456 ANI61C3825: 375735	25662 ENU09457 ANI61C5283: 954108	25663 ENU09458 ANI61C5286: 531786	25664 ENU09459 ANI61C4559: 151684

# corece certaine

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25665 ENU09460 ANI61S4392: 18500	Selection Basis GTBX	Database Hit ncbi gi "AFUc01686, Y13138"	aat Blast Blast Score Score Prob "1.1e-43,	% % id cvrg Description 13,
25666 ENU09461 ANI61C4561: 27754	GTBX	"AFUc10269, FGRc22925"	"3.0e-23, 2.5e-28"	23, 8"
25667 ENU09462 ANI61C3833: 646232	GTBX	FGRc04710	8.2E-72	2
25668 ENU09463 ANI61C3834: 11671727	GTBX	AFUc16457	3.3E-29	6
25669 ENU09464 ANI61C5294: 1041654	GTBX	"AFUc15936, FGRc11101"	"1.2e- 123, 5.2e-24"	<u>-</u>
25670 ENU09465 ANI61S3674: 2708	GTBX	AFUc10670	8.6E-33	3
25671 ENU09466 ANI61C3840: 162656	GTBX	"AFUc18322, AFUc21010"	"1.7e-19, 2.1e-26"	19, 6"
25672 ENU09467 ANI61C4570: 22853385	GTBX	AFUc17804	1.3E-21	.1
25673 ENU09468 ANI61C4585: 98330	GTBX	Y13135	4.5e-64	4
25674 ENU09469 ANI61C4589: 727290	GTBX	AFUc21610	2E-25	
25675 ENU09470 ANI61C3869: 25390	GTBX	AFUc08072	4.6E-43	.3
25676 ENU09471 ANI61C4599: 54440	GTBX	AFUc08426	1.4E-25	S
25677 ENU09472 ANI61C3870: 791270	GTBX	CALc05830	2.9E-34	4
25678 ENU09473 ANI61C3877: 13841001	GTBX	AFUc01915	1.9E-47	7

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Seq num Seq id Contig source 25679 ENU09474 ANI61C3878 1289596	Contig source ANI61C3878: 1289596	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "CALc04339, FGRc02339"	aat Blast Score Score	Blast Prob "4.4e-76, 3.3e-84"	% id cvrg Description
25680 ENU09475 ANI61C3879: 68479	ANI61C3879: 68479			GTBX	AFUc09507		2.3E-40	
25681 ENU09476 ANI61C38 785207	ANI61C3881: 785207			GTBX	CALc03328		5.8E-44	
25682 ENU09477 ANI61C3888: 813247	ANI61C3888: 813247			GTBX	AFUc05510		6.2E-28	
25683 ENU09478 ANI61C3889: 1158606	ANI61C3889: 1158606			GTBX	AFUc13973		9.9E-73	
25684 ENU09479 ANI61C3893: 13733	ANI61C3893: 13733			GTBX	"AFUc04394, AFUc14651"		"8.1e-41, 2.6e-96"	
25685 ENU09480 ANI61C3895: 540755	ANI61C3895: 540755			GTBX	AFUc12362		1.1E-54	
25686 ENU09481 ANI61C9601: 71487954	ANI61C9601: 71487954			GTBX	AFUc17920		5.3E-44	
25687 ENU09482 ANI61C9605: 103250	ANI61C9605: 103250			GTBX	AFUc12404		5.5E-76	
25688 ENU09483 ANI61C9609: 1184573	ANI61C9609: 1184573			GTBX	"AFUc12674, AFUc16179, FGRc06836"		"7.5e-22, 5.1e-25, 3.7e-61"	
25689 ENU09484 ANI61C9611: 1087208	ANI61C9611: 1087208			GTBX	CALc04433		2.7E-99	
25690 ENU09485 ANI61C9621: 20171559	ANI61C9621: 20171559			GTBX	AFUc01710		9.7E-47	
25691 ENU09486 ANI61C9624: 12871999	ANI61C9624: 12871999			GTBX	"AFUc04270, AFUc04681, AFUc04681"		"2.7e-49, 1.4e-28, 2.4e-35"	
25692 ENU09487 ANIGIC8901: 18822697	ANI61C8901: 18822697			GTBX	AFUc13517		4.7E-78	

# nguen centration

aat Blast Blast % Score Score Prob % id cvrg Description "5.8e-09, 7.4e-37"	1.2E-36	4.3E-66	1.5E-46	"1.5e-35, 8.5e-29"	5.7E-79	"6.5e-69, 4.9e- 120, 4.2e-12, 1.6e-10"	3.3E-29	"1.3e-35, 3.3e-29, 8.8e-22"	4E-40	"2.4e-13, 2.3e- 140"	1.0e-14	"1.0e-83, 4.3e- 149"
tion  Database Hit ncbi gi  X "AFUc20792, FGRc07150"	X AFUc09350	X AFUc09871	X AFUc15919	X "AFUc01729, FGRc17590"	X AFUc08511	X "AFUc04955, AFUc09378, FGRc08438, FGRc21707"	X AFUc08746	X "AFUc02649, CALc04199, CALc04199"		X "AFUc04650, CALc04969"	X Y13138	X "AFUc10881, Y13139"
ner Primer Selection ss 3 pos Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Seq Primer num Seq id Contig source 5 pos 25693 ENU09488 ANI61C9632: 651007	25694 ENU09489 ANI61C9634: 83697788	25695 ENU09490 ANI61C9635: 21932786	25696 ENU09491 ANI61C8908: 28913656	25697 ENU09492 ANI61C9638: 42707025	25698 ENU09493 ANI61C9639: 14251036	25699 ENU09494 ANI61C9640: 2603911	25700 ENU09495 ANI61C9642: 20351577	25701 ENU09496 ANI61C8922: 129531	25702 ENU09497 ANI61C8922: 35302993	25703 ENU09498 ANI61C9657: 38652196	25704 ENU09499 ANI61C9658: 76128	25705 ENU09500 ANI61C9664: 22414059

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25706 ENU09501 ANI61C9669: 37835102	ner Selection os Basis GTBX	Database Hit ncbi gi "AFUc10037, AFUc12096"	aat Blast Bl Score Score Pr "1	Blast % Prob % id cvrg Description "1.4e-95, 5.2e-40"
25707 ENU09502 ANI61C8941: 564836	GTBX	AFUc07937	1.1	1.5E-56
25708 ENU09503 ANI61C9675: 2597749	GTBX	"AFUc10109, AFUc17198, AFUc17198, FGRc15837, FGB.25158	E. 4. 2	"3.0e-78, 4.0e-21, 5.3e-23, 1.5e-21, 3.5e-13"
25709 ENU09504 ANI61C9677: 20101543	GTBX	AFUc12413	. T	1.7E-102
25710 ENU09505 ANI61C8954: 683447	GTBX	AFUc08873	9	6.9E-34
25711 ENU09506 ANI61C9687: 8292	GTBX	"FGRc12006, Y13136"	"1 5.	"1.2e-51, 5.3e-40"
25712 ENU09507 ANI61C9691: 21151211	GTBX	AFUc05215	5.	5.3E-41
25713 ENU09508 ANI61C9692: 1160606	GTBX	AFUc16896	.2	2.9E-28
25714 ENU09509 ANI61C9694: 44903594	GTBX	"AFUc20993, U00092"	3. 3.	"2.6e-46, 3.6e-07"
25715 ENU09510 ANI61C8966: 57536363	GTBX	"AFUc06989, Z71256"	<sub>4</sub> 4.	"4.3e-36, 4.6e-11"
25716 ENU09511 ANI61C9695: 92372	GTBX	"AFUc14005, AFUc20315"	3.	"7.8e-29, 3.3e-73"
25717 ENU09512 ANI61C8967: 28262269	GTBX	AFUc03802	4	4.7E-40
25718 ENU09513 ANI61C8971: 1468733	GTBX	"CALc05073, FGRc02949"	". 7.	"1.2e-22, 7.5e-24"

# compand no se

Seq num Seq id Contig source 25719 ENU09514 ANI61C8973: 5741417	Contig source ANI61C8973: 5741417	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc21866	aat Blast Score Score	Blast Prob % i 1.9E-30	% id cvrg Description
25720 ENU09515 ANI61C8979: 129506	ANI61C8979: 129506			GTBX	AFUc00391		5.9E-29	
25721 ENU09516 ANI61C8979: 34113851	ANI61C8979: 34113851			GTBX	AFUc05896		9.6E-24	
25722 ENU09517 ANI61C6002: 18301440	ANI61C6002: 18301440			GTBX	AFUc13365		4.5E-61	
25723 ENU09518 ANI61C6003: 10161437	ANI61C6003: 10161437			GTBX	AFUc14299		3.9E-71	
25724 ENU09519 ANI61C8982: 7562038	ANI61C8982: 7562038			GTBX	"AFUc09202, Y13139"		"6.1e-92, 1.1e-28"	
25725 ENU09520 ANI61C8987: 57185065	ANI61C8987: 57185065			GTBX	FGRc14942		2.8E-33	
25726 ENU09521 ANI61C8988: 291003	ANI61C8988: 291003			GTBX	"AFUc09518, FGRc00963"		"4.6e-37, 8.8e-14"	
25727 ENU09522 ANI61C6010: 705413	ANI61C6010: 705413			GTBX	AFUc11775		3.6E-69	
25728 ENU09523 ANI61C8992: 10601268	ANI61C8992: 10601268			GTBX	AFUc15788		6.5E-46	
25729 ENU09524 ANI61C6023 22959	ANI61C6023: 22959			GTBX	AFUc08361		2.1E-105	
25730 ENU09525 ANI61C6028: 698112	ANI61C6028: 698112			GTBX	AFUc15445		2.8E-45	
25731 ENU09526 ANI61C5302 8041978	ANI61C5302: 8041978			GTBX	"AFUc03529, FGRc15568,		"3.9e-75, 1.9e-31,	
25732 ENU09527 ANI61C6032: 121656	ANI61C6032: 121656			GTBX	FGRc24538		5.3E-24	

aat Blast Blast % Score Score Prob % id cvrg Description "4.1e-46, 1.3e-	1.7E-36	1.3E-22	1.5E-54	"1.4e-19, 7.9e-53, 3.2e-50"	"3.1e-46, 1.8e-07"	6.7E-28	"4.3e-88, 4.4e-20"	9.2E-73	9.1E-40	"5.1e-54, 1.9e-34, 7.7e-11, 5.1e-13"	3.2E-30	4.1E-82	"8.4e-62, 1.9e-72"
n Database Hit ncbi gi "CALc04320, CALc06192"	AFUc13255	AFUc14608	AFUc08453	"AFUc20402, CALc05987, FGBc05827"	"AFUc20512, CALc05290"	CALc05007	"AFUc11807, FGRc09518"	AFUc08478	AFUc01410	"AFUc06920, AFUc07230, AFUc14567, V13135"	AFUc13039	AFUc07396	"AFUc21842, CALc05774"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos													
Primer 5 pos											••		••
Seq num Seq id Contig source 25733 ENU09528 ANI61C5304: 201813	25734 ENU09529 ANI61C5307: 1011634	25735 ENU09530 ANI61C6040: 498238	25736 ENU09531 ANI61C5312: 17463	25737 ENU09532 ANI61C6044: 827423	25738 ENU09533 ANI61C5317: 3599	25739 ENU09534 ANI61C5320: 38324	25740 ENU09535 ANI61C5322: 2464874	25741 ENU09536 ANIGLC5323: 5571220	25742 ENU09537 ANI61C6052: 840342	25743 ENU09538 ANI61C5324: 154758	25744 ENU09539 ANI61C6062: 37739	25745 ENU09540 ANI61C4610: 78674	25746 ENU09541 ANI61C5341: 144135

% id cvrg Description								•				
Blast Prob 7.4e-89	"2.3e-18, 2.3e-22"	1.5E-44	5.3E-47	1.1E-35	4.5E-46	2E-30	3E-56	"1.0e-23, 6.0e-13"	1.3E-42	2.9E-89	7.3E-30	"1.3e-71, 3.5e-44, 3.5e-75, 2.7e-29, 1.3e-68"
Blast E Score F	: 0	-	Ψ)	-	4	(1	(1)	. 0		(1		
Score												
Database Hit ncbi gi Y13137	"AFUc04409, AFUc14023"	FGRc11453	AFUc22404	AFUc02673	AFUc19745	AFUc12813	AFUc10825	"AFUc14213, CALc06077"	AFUc00550	AFUc08943	AFUc05917	"AFUc17196, AFUc18488, AFUc18488, FGRc00704, Y13134"
	"AFT AFU	FGR	AFU	AFU	AFU	AFU	AFU	"AFT CAL	AFU		AFU	"AFU AFU AFU FGR Y13
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos												
Primer 5 pos												
Seq id Contig source 7 ENU09542 ANI61C6074: 1430126	25748 ENU09543 ANI61C5348: 204149	25749 ENU09544 ANI61C5351: 37062627	25750 ENU09545 ANI61C5355: 40077	25751 ENU09546 ANI61C5363: 19862330	25752 ENU09547 ANI61S3748: 25508	25753 ENU09548 ANI61C3914: 1336	25754 ENU09549 ANI61C5372: 27823320	25755 ENU09550 ANI61C4644: 385122	25756 ENU09551 ANI61C3915: 1063782	25757 ENU09552 ANI61C5373: 61136	25758 ENU09553 ANI61C5376: 55480	25759 ENU09554 ANI61C3920: 224756
Seq num 25747	25	25	25	25	25	25	25	25	25	25	25	25

# cester ceretain

Seq num Seq id 25760 ENU09555	Contig source ANI61C4650: 13722	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi "AFUc14849, FGRc00854"	aat Blast Score Score	Blast Prob 9 "3.1e-10, 6.0e-32"	% % id cvrg Description	
25761 ENU09556 ANI61C4651: 87050	ANI61C4651: 87050			GTBX	"AFUc22660, FGRc07303"		"6.5e-29, 3.2e-52"		
25762 ENU09557 ANI61C4652: 7522207	ANI61C4652: 7522207			GTBX	AFUc14076		8.4E-46		
25763 ENU09558 ANIGLC5381: 1004492	ANI61C5381: 1004492			GTBX	AFUc03475		4.2E-51		
25764 ENU09559 ANI61C3925: 218802	ANI61C3925: 218802			GTBX	AFUc15140		9.4E-57		
25765 ENU09560 ANI61C5385: 15511769	ANI61C5385: 15511769			GTBX	AFUc07950		2.4E-42		
25766 ENU09561 ANI61C4657: 42236270	ANI61C4657: 42236270			GTBX	"AFUc11820, AFUc12573, AFUc14610, Y13135"		"5.1e- 145, 4.5e-84, 1.4e-15, 2.0e-98"		
25767 ENU09562 ANI61C3 51428	ANI61C3929: 51428			GTBX	AFUc01963		1.3E-45		
25768 ENU09563 ANI61C5387: 1209723	ANI61C5387: 1209723			GTBX	FGRc03431		5.6E-46		
25769 ENU09564 ANI61C465	. ANI61C4659: 10121228			GTBX	AFUc14550		3.7E-25		
25770 ENU09565 ANI61C5 2432208	ANI61C5388: 24322081			GTBX	"AFUc11974, AFUc14576"		"3.6e-40, 2.4e-67"		
25771 ENU09566 ANI61C5389: 97686	ANI61C5389: 97686			GTBX	AFUc10526		-1.7E-51		
25772 ENU09567 ANI61C4663: 149637	ANI61C4663: 149637			GTBX	AFUc14674		1.6E-25		

aat Blast Blast % Score Score Prob % id cvrg Description "1.0e-81, 2.1e-79, 3.6e-	2.6E-26	"2.3e- 103, 3.5e-33"	5.6E-33	3.2E-32	"2.5e-36, 8.9e-30"	3.4E-35	"6.9e-43, 3.0e-21"	3.5E-65	"1.7e-18, 1.8e-36"	"2.6e-83, 2.5e-47"	"1.9e-90, 5.3e-42"	"8.1e-28, 9.6e-37"	"6.3e-14, 7.6e- 171"
Selection Basis Database Hit ncbi gi GTBX "AFUc05105, AFUc11030, FGRc07318"	GTBX FGRc10474	GTBX "AFUc09487, FGRc08263"	GTBX AFUc15972	GTBX AFUc13983	GTBX "AFUc00630, AFUc16315"	GTBX AFUc11129	GTBX "AFUc15086, Y13138"	GTBX AFUc14919	GTBX "AFUc19250, Y13138"	GTBX "AFUc13453, FGRc11821"	GTBX "AFUc00727, AFUc21727"	GTBX "AFUc02588, AFUc02588"	GTBX "AFUc19352, CALc06116"
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 25773 ENU09568 ANI61C5396: 12073398	25774 ENU09569 ANI61C4667: 42234	25775 ENU09570 ANI61C4669: 6968	25776 ENU09571 ANI61C5399: 1944519	25777 ENU09572 ANI61C4672: 742473	25778 ENU09573 ANI61C3953: 2205895	25779 ENU09574 ANI61C4683: 43536	25780 ENU09575 ANI61C3956: 1317362	25781 ENU09576 ANI61C3965: 26162940	25782 ENU09577 ANI61C3966: 9241	25783 ENU09578 ANI61C4698: 6511923	25784 ENU09579 ANI61C3971: 104834	25785 ENU09580 ANI61C3972: 36392620	25786 ENU09581 ANI61C3973: 2117461

## communica communica

aat Blast Blast % ncbi gi Score Score Prob % id cvrg Description 2.9E-166	6.4E-34	1.1E-28	"1.9e-51, 1.4e-46, 1.6e-11"	2E-26	1.7E-29	"2.0e-14, 1.2e-43"	2.6E-31	7.3E-108	9.9E-36	"5.0e-52, 1.3e-12"	5.9E-121	"2.8e-32, 5.4e-26"	8.2E-69
Database Hit no AFUc15344	FGRc04709	AFUc08610	"AFUc01633, AFUc19340, ECP c18569"	AFUc02769	AFUc20274	"AFUc05280, AFUc21291"	AFUc14424	AFUc14916	AFUc10051	"AFUc14099, FGRc00303"	AFUc08909	"AFUc03916, AFUc06334"	AFUc12163
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 5 25787 ENU09582 ANI61C3977: 1953643	25788 ENU09583 ANI61C3978: 84382	25789 ENU09584 ANI61C1002: 26112219	25790 ENU09585 ANI61C1003: 2507993	25791 ENU09586 ANI61C1014: 740199	25792 ENU09587 ANI61C3992: 282521	25793 ENU09588 ANI61C3995: 44766	25794 ENU09589 ANI61C1022: 766454	25795 ENU09590 ANI61C1025: 55632	25796 ENU09591 ANI61C1030: 37573323	25797 ENU09592 ANI61C1038: 7121006	25798 ENU09593 ANI61C1044: 190335	25799 ENU09594 ANI61C1052: 1095102	25800 ENU09595 ANI61C1053: 618115

Primer Primer Selection 5 pos 3 pos Basis Database Hit ncbi gi Score Score GTBX "AFUc17783,	606 8.3e-23" VIGIC1058: GTBX AFUc12718 4.7E-23	VIGIC1069: GTBX AFUc15622 1.1E-58 505330	VIGIC9702: GTBX "AFUc18380, "8.9e-49, CALc02515, 7.3e-93, U00092" 1.5e-	GTBX AFUc10199	VI61C9706: GTBX "CALc05544, "3.8e- 616696 Y13137" 234, 3.7e-	17: GTBX "AFUc05673, AFUc07215"	GTBX AFUc18240	NI61C1084: GTBX AFUc14920 1.2E-23	NI61C9720: GTBX "AFUc12550, "3.7e- 61467 CALc05628" 168,	GTBX "AFUc03966, FGRc09117"	NI61C9733: GTBX AFUc14559 2.3E-43	
source C1056:	1606 25802 ENU09597 ANI61C1058: 26062340	25803 ENU09598 ANI61C1069: 49505330	25804 ENU09599 ANI61C9702: 2851385	25805 ENU09600 ANI61C9702: 44614919	25806 ENU09601 ANI61C9706: 48616696	25807 ENU09602 ANI61C9717: 4191280	25808 ENU09603 ANI61C9718: 618277	25809 ENU09604 ANI61C1084: 317835	25810 ENU09605 ANI61C9720: 3561467	25811 ENU09606 ANI61C1095: 41664419	25812 ENU09607 ANI61C9733: 23092918	

### corca canda

Seq num Seq id Contig source 25814 ENU09609 ANI61C9739: 74407764		Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc20780	aat Blast Score Score	Blast Prob 3E-49	% id cvrg Description
25815 ENU09610 ANI61C9743: 1418873	ANI61C9743: 1418873			GTBX	"CALc05775, FGRc05013"		"2.8e-60, 1.9e-26"	
25816 ENU09611 ANI61C9752: 128351	ANI61C9752: 128351			GTBX	"AFUc14599, CALc02009"		"8.4e- 132,	
25817 ENU09612 ANI61C9760: 36674155	ANI61C9760: 36674155			GTBX	AFUc07682		1.8E-31	
25818 ENU09613 ANI61C9760: 58724366	ANI61C9760: 58724366			GTBX	"AFUc07479, Y13134"		"2.6e-66, 1.2e-55"	
25819 ENU09614 ANI61C9769: 120994	ANI61C9769: 120994			GTBX	AFUc07018		5.2E-44	
25820 ENU09615 ANI61C9773: 1037200	ANI61C9773: 1037200			GTBX	"AFUc08480, FGRc23544"		"3.2e-16, 1.7e-34"	
25821 ENU09616 ANI61C9775: 13642760	ANI61C9775: 13642760			GTBX	"AFUc06544, AFUc15485"		"3.2e-35, 6.5e-73"	
25822 ENU09617 ANI61C9790: 4153897	ANI61C9790: 4153897			GTBX	"AFUc02169, AFUc12397, CALc01597, CALc04669"		"2.0e-70, 2.3e-252, 5.0e-19, 9.6e-	
25823 ENU09618 ANI61C9792: 540156	ANI61C9792: 540156			GTBX	AFUc09788		5.2E-45	
25824 ENU09619 ANI61C9794: 33492897	ANI61C9794: 33492897			GTBX	AFUc09569		1.8E-27	
25825 ENU09620 ANI61C6100: 325100	ANI61C6100: 325100			GTBX	AFUc06484		2.5E-26	

# certon cerucion

aat Blast % % Score Score Prob % id cvrg Description "1.7e-54, 3.0e-53, 8.0e-14,	2.5E-48	5.3E-71	1.3E-80	4.2E-24	5.8E-49	1.4E-51	1.5e-38	"9.1e-23, 8.7e-11"	"2.5e-37, 3.4e- 110"	"1.9e-28, 1.8e-07, 2.7e-13"	3.8E-31	"1.2e-18, 1.3e-21"	"9.8e-61, 2.0e-47"
Selection Basis Database Hit ncbi gi GTBX "AFUc10825, AFUc14691, AFUc15224,	GTBX AFUc09931	GTBX FGRc04110	GTBX CALc05352	GTBX AFUc07714	GTBX FGRc05103	GTBX AFUc01942	GTBX Y13135	GTBX "AFUc00820, Z71256"	GTBX "AFUc05916, CALc05479"	GTBX "AFUc04896, AFUc05822, FGRc10423"	GTBX AFUc07579	GTBX "AFUc01051, FGRc10010"	GTBX "AFUc04407, FGRc10921"
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25826 ENU09621 ANI61C6108: 2081945	25827 ENU09622 ANI61C6109: 214997	25828 ENU09623 ANI61C6112: 97584	25829 ENU09624 ANI61C6113: 8928	25830 ENU09625 ANI61C6129: 4231525	25831 ENU09626 ANI61S4500: 36367	25832 ENU09627 ANI61C6132: 403107	25833 ENU09628 ANI61S4517: 45440	25834 ENU09629 ANI61C6140: 511322	25835 ENU09630 ANI61C6142: 1192107	25836 ENU09631 ANI61C6146: 15902326	25837 ENU09632 ANI61C5425: 70294	25838 ENU09633 ANI61C6154: 7021596	25839 ENU09634 ANI61C5426: 76112

### nouncer company

Seq num Seq id 25840 ENU09635	Contig source ANI61C6157: 20881205	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc14533	aat Blast Bl Score Score Pr 6.	Blast % Prob % id cvrg Description 6.7E-30
25841 ENU09636 ANI61C4701: 814374	ANI61C4701: 814374			GTBX	"AFUc05559, FGRc08592"		"3.7e-89, 2.2e-25"
25842 ENU09637 ANI61C5430: 1315803	ANI61C5430: 1315803			GTBX	AFUc10737	1.1	1.5E-23
25843 ENU09638 ANI61C4705: 151511	ANI61C4705: 151511			GTBX	AFUc13476		2.4E-72
25844 ENU09639 ANI61C5435: 95861	ANI61C5435: 95861			GTBX	AFUc14400	-1	1.5E-50
25845 ENU09640 ANI61C5440: 123415	ANI61C5440: 123415			GTBX	U00093	1	1.4e-111
25846 ENU09641 ANI61C4712: 6061352	ANI61C4712: 6061352			GTBX	AFUc01145		6.8E-39
25847 ENU09642 ANI61C6171: 1210226	ANI61C6171: 1210226			GTBX	AFUc15787	.8	5.9E-33
25848 ENU09643 ANI61C5442: 17381020	ANI61C5442: 17381020			GTBX	AFUc02895	1.	1.5E-36
25849 ENU09644 ANI61C5444: 320668	ANI61C5444: 320668	:.		GTBX	AFUc15322	11	1E-37
25850 ENU09645 ANI61C4716: 32353650	ANI61C4716: 32353650			GTBX	AFUc13372	.5.	5.7E-52
25851 ENU09646 ANI61C5449: 3537	ANI61C5449: 3537			GTBX	AFUc15317	1.	1.1E-27
25852 ENU09647 ANI61S3822: 109415	ANI61S3822: 109415			GTBX	AFUc05500	4	4.6E-31
25853 ENU09648 ANI61C4720: 32475	ANI61C4720 32475			GTBX	AFUc04498	51	5E-36

### COLUMNIC COLUMNIC

Blast Blast % Score Prob % id cvrg Description "1.9e-74, 1.0e-48"	2.5E-22	2.7E-37	5.1E-45	4.4E-39	"4.9e-21, 4.5e-14"	"2.5e- 144, 3.4e-13"	"1.9e-11, 1.6e-55, 1.6e-48"	"1.1e-22, 1.2e-46"	4.5E-69	"3.2e-21, 5.2e-22"	2.7E-62	5.2E-105	4.2E-61
aat Bl Score Sc													
Database Hit ncbi gi "AFUc08234, AFUc14268"	AFUc21338	FGRc06110	AFUc06221	AFUc12008	"AFUc16901, FGRc10006"	"AFUc09040, AFUc14490"	"AFUc07396, AFUc11792, AFUc14619"	"AFUc14839, CALc04948"	AFUc13184	"AFUc06054, AFUc20036"	AFUc14106	AFUc11624	AFUc13777
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 5 25854 ENU09649 ANI61C4721: 17732670	25855 ENU09650 ANI61C5451: 502849	25856 ENU09651 ANI61C6182: 644.27	25857 ENU09652 ANI61C5454: 2340	25858 ENU09653 ANI61C4727: 336664	25859 ENU09654 ANI61C5456: 112655	25860 ENU09655 ANI61C6187: 1320540	25861 ENU09656 ANI61C5458: 5711412	25862 ENU09657 ANI61C4730: 1349868	25863 ENU09658 ANI61C6190: 1462	25864 ENU09659 ANI61C5464: 911132	25865 ENU09660 ANI61C4738: 66633	25866 ENU09661 ANI61C4739: 8592	25867 ENU09662 ANI61C6199: 9091228

# nounce nemen

aat Blast Blast % Score Score Prob % id cvrg Description 1.9E-25	1.3E-96	9E-52	"1.8e-20, 2.2e-21"	2.5E-26	1.2E-119	8.9E-37	"1.5e- 107, 1.5e-17"	2.2E-21	1.3E-26	1.2E-26	3.3E-42	2.2E-125	"4.3e-41, 5.1e-29"
Database Hit ncbi gi AFUc22120	AFUc10405	AFUc05296	"AFUc01962, AFUc11850"	AFUc01962	AFUc14868	AFUc11381	"AFUc08610, AFUc16734"	AFUc02287	AFUc14997	AFUc02466	AFUc02766	AFUc11383	"AFUc15660, FGRc09694"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq Pour Sed id Contig source 5 25868 ENU09663 ANI61C4741: 506156	25869 ENU09664 ANI61C4742: 73894	25870 ENU09665 ANI61C5472: 11351935	25871 ENU09666 ANI61C5475: 13.408	25872 ENU09667 ANI61C5475: 1314662	25873 ENU09668 ANI61C4748: 12152511	25874 ENU09669 ANI61C5479: 620144	25875 ENU09670 ANI61C5479: 11892303	25876 ENU09671 ANI61C4756: 40733	25877 ENU09672 ANI61S3867: 266498	25878 ENU09673 ANI61C4761: 56845	25879 ENU09674 ANI61S3872: 44665	25880 ENU09675 ANI61C4771: 110962	25881 ENU09676 ANI61C4786: 876135

Blast Blast %  ce Score Prob % id cvrg Description 2.5e-14	1.1E-44	"2.2e-78, 8.8e-38, 8.5e-29"	2.7E-37	"6.4e-87, 2.8e-40"	"3.0e-09, 4.3e-35"	"1.2e-22, 8.1e-09, 2.3e-56, 3.5e-13,	1.36-41	"2.0e-58, 5.5e-76, 2.5e-19, 1.8e-	"9.7e-40, 5.8e-17"	"2.3e- 128, 4.6e- 111, 5.8e-73, 4.3e- 166"
aat Database Hit ncbi gi Score Y13134	AFUc13817	"AFUc09124, AFUc09640, AFIL18058"	FGRc09135	"AFUc15843, U00094"	"AFUc00779, FGRc22503"	"AFUc03712, AFUc18769, CALc03518, FGRc12834,	134	"AFUc00718, AFUc10854, AFUc11508, Z71256"	"AFUc10316, AFUc22327"	"AFUc08048, AFUc09981, FGRc03735, Y13136"
r Selection Basis GTBX	GTBX AFUc	GTBX "AFU AFU	GTBX FGRe	GTBX "AFUC15 U00094"	GTBX "AFU FGRo	GTBX "AFU AFU CALA FGRA	GTBX Y13134	GTBX "AFUc00 AFUc108 AFUc115 Z71256"	GTBX "AFU AFU	GTBX "AFU AFU FGR Y131
Primer Primer 5 pos 3 pos :								·		21
Seq num Seq id Contig source 25882 ENU09677 ANI61C4789: 204437	25883 ENU09678 ANI61C4789: 1071690	25884 ENU09679 ANI61C4797: 3192529	25885 ENU09680 ANI61C1103: 26999	25886 ENU09681 ANI61C1105: 13573	25887 ENU09682 ANI61C1111: 59006720	25888 ENU09683 ANI61C1120: 1023112501	25889 ENU09684 ANI61C1121: 48473694	25890 ENU09685 ANI61C1123: 295923	25891 ENU09686 ANIGIC1126: 20541083	25892 ENU09687 ANI61C1132: 33626968

### Corcect Caron

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25893 ENU09688 ANI61C1132: 79608202	Selection Basis GTBX	Database Hit ncbi gi AFUc12080	aat Blast Blast Score Score Prob 3.2E-	Blast % Prob % id cvrg Description 3.2E-39
25894 ENU09689 ANI61C1133: 37015484	GTBX	"AFUc16469, Y13137"	. <sup>9</sup> .	"9.6e-37, 1.2e-44"
25895 ENU09690 ANI61C1133: 68975740	GTBX	FGRc03896	5.8	5.8E-55
25896 ENU09691 ANI61C1138: 1214010469	GTBX	"AFUc13136, CALc04542"	"8.4e 121, 3.5e-3	"8.4e- 121, 3.5e-38"
25897 ENU09692 ANI61C1141: 13831990	GTBX	"AFUc22467, FGRc06420"		"1.9e-71, 5.1e-08"
25898 ENU09693 ANI61C1142: 1359266	GTBX	AFUc15387	2.7	2.7E-96
25899 ENU09694 ANI61C1145: 338979	GTBX	"AFUc21496, Y131340"		"2.0e-58, 1.8e-12"
25900 ENU09695 ANI61C1147: 34484162	GTBX	"AFUc06122, CALc05976, FGR.03662"	1. 4.6	"1.7e-27, 4.0e-52, 7.5e-53"
25901 ENU09696 ANI61C1156: 74937059	GTBX	AFUc13989	5.5	5.7E-25
25902 ENU09697 ANI61C1161: 553281	GTBX	FGRc16793	[1	1.1E-44
25903 ENU09698 ANI61C9802: 38782312	GTBX	"FGRc12359, FGRc26682, Y13140"	5.2 5.4	"5.3e-08, 5.2e-13, 4.4e-67"
25904 ENU09699 ANI61C9804: 1241151	GTBX	AFUc03380	2E	2E-46
25905 ENU09700 ANI61C1178: 87853	GTBX	AFUc03777	3.4	3.4E-26
25906 ENU09701 ANI61C9810: 17561256	GTBX	FGRc23086	- T	1.1E-24

% % id cvrg Description )	. =	£_		ر د د		84	31	4	% <b>.</b>	5	2	5,	1, 9"
Blast Prob 1.5E-60	"2.1e- 170, 2.6e-21,	"0.0, 2.6e-30"	8.4E-43	"1.2e-45, 5.9e-08, 2.4e-27"	8.2E-33	1.7E-184	2.4E-131	8.1E-24	"3.5e-28, 2.1e-19, 6.1e-18"	"2.2e-16, 3.8e-23"	8.4E-22	"2.9e-45, 4.7e-53"	"4.6e-31, 6.7e-19"
Blast Score													
aat Score													
ncbi gi													
Database Hit FGRc06851	"AFUc10035, FGRc20878, Y13136"	"AFUc15897, CALc05493"	AFUc08928	"AFUc04073, AFUc20231, AFTC21886"	AFUc13521	AFUc15367	CALc05806	AFUc09714	"AFUc11109, AFUc17602, FGRc08107"	"AFUc14827, CALc04616"	AFUc08740	"AFUc11344, AFUc11344"	"AFUc12331, AFUc21805"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 25907 ENU09702 ANI61C1180: 11962056	25908 ENU09703 ANI61C1183: 223721	25909 ENU09704 ANI61C1186: 5213806	25910 ENU09705 ANI61C1187: 41405351	25911 ENU09706 ANI61C1189: 77856298	25912 ENU09707 ANI6LC9824: 51134670	25913 ENU09708 ANI61C9826: 11518	25914 ENU09709 ANI61C9830: 1703409	25915 ENU09710 ANIGIC9830: 5218.4379	25916 ENU09711 ANI61C9834: 65717561	25917 ENU09712 ANI61C9836: 947226	25918 ENU09713 ANI61C9839: 611879	25919 ENU09714 ANIGIC9847: 19862857	25920 ENU09715 ANI61C9847: 42643095

### counter correc

Seq		Primer	Primer	Selection		aat Blast Blast	%
num Seq id 25921 ENU09716	Contig source ANI61C9847: 928510497	sod 5	3 pos	Basis GTBX	Database Hit ncbi gi FGRc11572	Score Score Prob 9.4E-41	% id cvrg Description
25922 ENU09717 ANI61C9854: 36563	ANI61C9854: 36563			GTBX	AFUc20068	2.7E-30	-30
25923 ENU09718 ANI61C9864: 18012743	ANI61C9864: 18012743			GTBX	AFUc15416	9.7E-198	-198
25924 ENU09719 ANI61C9871: 463701	ANI61C9871: 463701			GTBX	AFUc15546	1.5E-69	69-
25925 ENU09720 ANI61C9873: 4962	ANI61C9873: 4962			GTBX	AFUc14820	2.7E-81	-81
25926 ENU09721 ANI61C9876: 2029906	ANI61C9876: 2029906			GTBX	AFUc13760	2.8E-81	-81
25927 ENU09722 ANI61C9880: 33651981	ANI61C9880: 33651981			GTBX	"AFUc06015, FGRc12116"	"6.3e-24, 8.9e-29"	≻24, 29"
25928 ENU09723 ANI61C9892: 1057687	ANI61C9892: 1057687			GTBX	"AFUc11408, FGRc01592"	"1.4e-98, 8.4e-10"	-98, 10"
25929 ENU09724 ANI61C6203: 1027511138	ANI61C6203: 1027511138			GTBX	AFUc13995	4.9E	4.9E-165
25930 ENU09725 ANI61C6205: 20781213	ANI61C6205: 20781213			GTBX	"AFUc15242, D50617"	"6.6e- 108, 1.2e-84"	***************************************
25931 ENU09726 ANI61C6213: 2259580	ANI61C6213: 2259580			GTBX	"AFUc02451, AFUc09901, CALc05142, Y13135"	"1.5e-95 2.4e-19, 6.3e-09, 1.5e-07"	"1.5e-95, 2.4e-19, 6.3e-09, 1.5e-07"
25932 ENU09727 ANI61C6227: 44833758	ANI61C6227: 44833758			GTBX	"AFUc03527, AFUc20765"	"2.4 3.1e	"2.4e-18, 3.1e-27"
25933 ENU09728 ANI61C5506: 20223044	ANI61C5506: 20223044			GTBX	AFUc15489	3.2E	3.2E-126
25934 ENU09729 ANI61C5507: 34703854	ANI61C5507: 34703854			GTBX	AFUc11680	1.2E-40	-40

### inderina inderination

Blast % Prob % id cvrg Description 5.8E-38	1.6E-47	9.8E-28	"1.5e-22, 8.3e-54"	7.6E-58	"5.6e-24, 2.1e-35, 2.8e-09"	3.2E-31	2.5E-68	1.8E-33	3.4E-35	7.1E-81	2.7E-74	2.5E-26	7.4E-25
aat Blast Score Score		σ,					.,			•		•	
Database Hit ncbi gi AFUc01334	AFUc06832	AFUc15836	"AFUc10347, AFUc15031"	AFUc13043	"AFUc01206, AFUc07147, FGRc12821"	AFUc15430	AFUc15185	AFUc06476	AFUc05360	AFUc05565	AFUc14753	AFUc09678	AFUc11585
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 25935 ENU09730 ANI61C6240: 4483	25936 ENU09731 ANI61C6242: 666250	25937 ENU09732 ANI61S4625: 238496	25938 ENU09733 ANI61C6254: 20362560	25939 ENU09734 ANI61C5528: 608123	25940 ENU09735 ANI61C4801: 11881772	25941 ENU09736 ANI61C5537: 605147	25942 ENU09737 ANI61C5537: 27862061	25943 ENU09738 ANI61C5542: 168530	25944 ENU09739 ANI61C4816: 33461	25945 ENU09740 ANI61C5549: 6151013	25946 ENU09741 ANI61C5552: 85193	25947 ENU09742 ANI61C6284: 673325	25948 ENU09743 ANI61S3933: 9233

Seq Primer Primer Primer num Seq id Contig source 5 pos 3 pos	r Selection Basis	Database Hit ncbi gi	aat Blast Blast Score Score Prob	% % id cvrg Description
23949 ENOU9/144 FUNIOIC+631. 45475	OID			
25950 ENU09745 ANI61C4836: 111215	GTBX	AFUc03302	8.9E-93	
25951 ENU09746 ANI61C4837: 4586	GTBX	AFUc08292	1.2E-92	
25952 ENU09747 ANI61C6297: 27433635	GTBX	"AFUc06848, Y13139"	"1.9e-76, 1.2e-25"	
25953 ENU09748 ANI61C6299: 14171637	GTBX	AFUc13847	2.2E-59	
25954 ENU09749 ANI61C4840: 108974	GTBX	AFUc13509	1.9E-118	
25955 ENU09750 ANI61C4849: 942589	GTBX	FGRc13511	4.8E-29	
25956 ENU09751 ANI61C5582: 44732	GTBX	CALc06150	6.4E-21	
25957 ENU09752 ANI61C5583: 5693	GTBX	AFUc20430	1.7E-25	
25958 ENU09753 ANI61C5586: 12962030	GTBX	"AFUc06713, FGRc18425"	"4.0e-57, 1.3e-09"	
25959 ENU09754 ANI61C4862: 28872038	GTBX	AFUc07470	1.2E-33	
25960 ENU09755 ANI61C4866: 1044484	GTBX	"AFUc08653, AFUc18008"	"7.0e-62, 1.6e-41"	
25961 ENU09756 ANI61C5596: 62342	GTBX	AFUc15561	6.3E-42	
25962 ENU09757 ANIG1C5598: 478113	GTBX	Y13137	1.3e-25	

### DOLLHED DOPES

Seq num Seq id 25963 ENU09758	Contig source ANI61C4874: 1487111	Primer 5 pos	Primer 3 pos	Selection Basis GTBX	Database Hit ncbi gi AFUc15142	aat Blast Score Score	Blast Prob 1.4E-124	% % id cvrg Description	
25964 ENU09759 ANI61C4	ANT61C4879: 18811163			GTBX	AFUc08813		1.9E-66		
25965 ENU09760 ANI61C4881: 1028::1734	ANI61C4881: 10281734			GTBX	FGRc13484		4E-30		
25966 ENU09761 ANI61C4882: 214776	ANI61C4882: 214776			GTBX	AFUc06352		2.3E-48		
25967 ENU09762 ANI61C4 511101	ANI61C4884: 511101			GTBX	FGRc04402		1.5E-33		
25968 ENU09763 ANI61C4887: 17831230	ANI61C4887: 17831230			GTBX	AFUc15282		6.9E-57		
25969 ENU09764 ANI61C4897: 3741395	ANI61C4897: 3741395			GTBX	"AFUc07714, AFUc07747, AFIC11389"		"2.0e-10, 2.8e-32, 5.6e-36"		
25970 ENU09765 ANI61C4899: 2581409	ANI61C4899: 2581409			GTBX	"AFUc12154, FGRc02884"		"3.8e-21, 3.2e-11"		
25971 ENU09766 ANI61S1 44214	ANI61S1039: 44214			GTBX	Y13140		3.5e-39		
25972 ENU09767 ANI61C 43787	ANI61C1205: 43787			GTBX	AFUc15751		1.5E-53		
25973 ENU09768 ANI61C1208: 63918168	ANI61C1208: 63918168			GTBX	"AFUc08640, AFUc14702"		"2.8e-95, 4.5e-16"		
25974 ENU09769 ANI61C1208: 876110056	ANT61C1208: 876110056			GTBX	"AFUc13639, CALc06164"		"5.6e- 119, 2.5e_26"		
25975 ENU09770 ANI61C1000 6:47814	ANI61C1000 6:47814			GTBX	AFUc08460		9.9E-21		
25976 ENU09771 ANI61C1000 7:188676	ANI61C1000 7:188676			GTBX	AFUc00879		2.6E-34		

aat Blast Blast % Score Score Prob % id cvrg Description 1.7E-68	7.3E-47	4.7E-29	1.9E-37	1.7E-35	"3.6e-52, 2.4e-39"	"1.5e-57, 1.2e-44"	"1.1e-74, 5.1e-52"	"7.6e-27, 3.8e-36, 2.4e-40"	1.1e- 155, 3.6e-09, 7.7e-30"	7.3E-23	2.7E-22	"1.1e- 166, 4.4e- 172, 1.0e-24"
Database Hit ncbi gi AFUc09190	AFUc14823	AFUc09627	AFUc10564	AFUc15919	"AFUc15619, FGRc18463"	"AFUc08495, AFUc15892"	"AFUc18869, CALc02488"	"AFUc11304, AFUc11498, AFTc15909"	"AFUc09022, AFUc11200, FGRc09828"	FGRc10845	FGRc03585	"CALc05504, CALc05504, FGRc10685"
Selection Basis GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX	GTBX
Primer Primer 5 pos 3 pos												
Seq num Seq id Contig source 25977 ENU09772 ANI61C1217: 53824258	25978 ENU09773 ANI61C1001 1:2557	25979 ENU09774 ANI61C1001 5:7312197	25980 ENU09775 ANI61C1223: 29752406	25981 ENU09776 ANI61C1226: 5114	25982 ENU09777 ANI61C1227: 1799965	25983 ENU09778 ANI61C1229: 1262913750	25984 ENU09779 ANI61C1002 0:14511	25985 ENU09780 ANI61C1002 5:14192136	25986 ENU09781 ANI61C1002 6:20604211	25987 ENU09782 ANI61C1002 8:8556	25988 ENU09783 ANI61C1234: 698264	25989 ENU09784 ANI61C1236: 3294247

### cornantalon

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 25990 ENU09785 ANI61C1003 9:78593	Selection Basis GTBX	Database Hit ncbi gi AFUc04205	aat Blast Score Score	Blast % Prob % id cvrg 2.2E-29	rg Description
25991 ENU09786 ANI61C1243: 76647	GTBX	AFUc14226		2.2E-47	
25992 ENU09787 ANI61C1244: 639205	GTBX	AFUc10187		4.6E-49	
25993 ENU09788 ANI61C1004 3:6381321	GTBX	AFUc11890		3.5E-128	
25994 ENU09789 ANI61C1004 3:45331878	GTBX	"AFUc18915, AFUc22245, CALc06125"		"2.9e-37, 5.4e-55, 6.3e-86"	
25995 ENU09790 ANI61S1082: 53381	GTBX	"AFUc14265, AFUc15053, CALc06148"		"3.6e-09, 1.1e-45, 1.8e-46"	
25996 ENU09791 ANI61C1004 8:12351896	GTBX	"AFUc17530, AFUc21626"		"9.1e-23, 4.6e-18"	
25997 ENU09792 ANI61S1086: 30622	GTBX	AFUc10933		2.8E-39	
25998 ENU09793 ANI61C1250: 965442	GTBX	AFUc02186		2.9E-64	
25999 ENU09794 ANI61C1251: 435235	GTBX	AFUc05890		1.8E-31	
26000 ENU09795 ANI61C1460: 658362	TBX	AFUc04191		1.4E-57	
26001 ENU09796 ANI61C1026 8:20162441	TBX	AFUc05348		1.5E-36	
26002 ENU09797 ANI61C1472: 23052820	TBX	AFUc15503		3.8E-62	
26003 ENU09798 ANI61C1473: 744469	TBX	AFUc05026		1.1E-51	

aat Blast Blast % Score Score Prob % id cvrg Description 1.1E-51	6.7E-37	3.7E-37	1.3E-129	7.2E-84	3.4E-59	1.7e-18	8.1E-69	1.5E-41	1.9E-35	1E-31	"1.7e-61, 4.9e-33"	1.4E-59	2.5E-53
Database Hit ncbi gi AFUc05026	AFUc13815	AFUc22069	AFUc14473	AFUc10944	AFUc14293	Y13138	AFUc08818	AFUc05906	CALc02816	AFUc14285	"AFUc11696, AFUc11696"	AFUc09975	AFUc12528
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 26004 ENU09799 ANI61C1473: 1063845	26005 ENU09800 ANI61C1027 6:15722084	26006 ENU09801 ANI61C1484: 26143107	26007 ENU09802 ANI61C1028 2:741950	26008 ENU09803 ANI61C1028 3:939666	26009 ENU09804 ANI61C1028 9:873166	26010 ENU09805 ANI61C322:2 3182686	26011 ENU09806 ANI61C349:9 9819772	26012 ENU09807 ANI61C352:5 2925651	26013 ENU09808 ANI61C363:3 042	26014 ENU09809 ANI61C7202: 134361	26015 ENU09810 ANI61C7216: 13901924	26016 ENU09811 ANI61C7219: 26452310	26017 ENU09812 ANI61C385:4 2604942

Seq num Seq id Contig 26018 ENU09813 ANI61 6664	source C388:4	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc20119	aat Blast Score Score	Blast Prob 1.2E-55	% id cvrg Description
26019 ENU09814 ANI61C7223: 29722172	ANI61C7223: 29722172			TBX	AFUc06424		1.1E-58	
26020 ENU09815 ANI61C7224: 44374850	ANI61C7224: 44374850			TBX	AFUc12875		3.1E-88	
26021 ENU09816 ANI61C7236: 14661086	ANI61C7236: 14661086			TBX	AFUc18591		3.4E-42	
26022 ENU09817 ANI61C7238: 680344	ANI61C7238: 680344			TBX	AFUc09528		2.5E-45	
26023 ENU09818 ANI61C7238: 1092832	ANI61C7238: 1092832			TBX	AFUc09528		2.5E-45	
26024 ENU09819 ANI61C7271: 1132605	ANI61C7271: 1132605			TBX	AFUc06636		2.4E-38	
26025 ENU09820 ANI61C7272 13711610	ANI61C7272: 13711610			TBX	AFUc07449		1.1E-44	
26026 ENU09821 ANI61C5818: 881339	ANI61C5818: 881339			TBX	AFUc08233		7.7E-38	
26027 ENU09822 ANI61 8127	ANI61S204:4 8127			TBX	FGRc12216		3.7E-40	
26028 ENU09823 ANI61C7285: 82488667	ANI61C7285: 82488667			TBX	AFUc15172		4.4E-69	
26029 ENU09824 ANI61C5830: 16802	ANI61C5830: 16802			TBX	AFUc08094		2.6E-48	
26030 ENU09825 ANI61C6560: 321156	ANI61C6560: 321156			TBX	AFUc13931		1.4E-79	
26031 ENU09826 ANI61C5832: 1096497	ANI61C5832: 1096497			TBX	AFUc08734		4.3E-50	

## nouter nervor

Seq num Seq id 26032 ENU09827	Contig source ANI61C5833: 38856	Primer 5 pos	Primer 3 pos	Selection Basis TBX	n Database Hit ncbi gi AFUc14136	aat Score	Blast Blast Score Prob 5.3E-62	% % id cvrg Description
26033 ENU09828 ANI61C5839: 16271427	ANI61C5839: 16271427			TBX	FGRc09504		1.8E-33	
26034 ENU09829 ANI61C5884: 2364	ANI61C5884: 2364			TBX	AFUc15412		1.3E-35	
26035 ENU09830 ANI61C5887: 9831786	ANI61C5887: 9831786			TBX	AFUc04019		2.4E-62	
26036 ENU09831 ANI61S 48060	ANI61S1313: 48060			TBX	AFUc15343		2E-56	
26037 ENU09832 ANI61C2211: 8621176	ANI61C2211: 8621176			TBX	AFUc14418		1.1E-61	
26038 ENU09833 ANI61C2212: 40522947	ANI61C2212: 40522947			TBX	"AFUc11116, AFUc12982"		"2.5e-97, 1.1e-57"	
26039 ENU09834 ANI61C2212: 4426.4133	ANI61C2212: 44264133			TBX	AFUc11116		2.5E-97	
26040 ENU09835 ANIGIC1103 1:22172515	ANI61C1103 1:22172515			TBX	AFUc13932		2.9E-51	
26041 ENU09836 ANI61C1030 2:139801419 5	ANI61C1030 2:139801419 5			TBX	AFUc15817		9.2E-172	2
26042 ENU09837 ANI61C1030 2:31972559	ANI61C1030 2:31972559			TBX	AFUc13294		4.2E-40	
26043 ENU09838 ANI61C1030 2:145981423	ANI61C1030 2:145981423			TBX	AFUc15817		4.4E-207	_
26044 ENU09839 ANI61C1103 2:58526235	ANI61C1103 2:58526235			TBX	"AFUc15294, AFUc22376,		"1.1e-91 2.0e-08,	
26045 ENU09840 ANI61C1103 7:24652914	ANI61C1103 7:24652914			TBX	AFUc01826		7.6E-34	

Seq num Seq id 26046 ENU09841	Contig source ANI61C2243: 32163	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc04253	aat Blast Score Score	Blast Prob 4.2E-93	% id cvrg Description
26047 ENU09842 ANI61C1031 8:68717170	ANI61C1031 8:68717170			TBX	AFUc08903		3E-41	
26048 ENU09843 ANI61C2250: 27.410	ANI61C2250: 27410			TBX	AFUc14478		8.6E-55	
26049 ENU09844 ANI61C1032 1:48025332	ANI61C1032 1:48025332			TBX	AFUc13535		1.4E-70	
26050 ENU09845 ANI61C1105 1:16501889	ANI61C1105 1:16501889			TBX	AFUc15849		3.5E-49	
26051 ENU09846 ANI61C1105 6:1393	ANI61C1105 6:1393			TBX	AFUc10621		4E-68	
26052 ENU09847 ANI61S 2411	ANI61S1369: 2411			TBX	AFUc15183		1.2E-41	
26053 ENU09848 ANI61C1033 0:13225	ANI61C1033 0:13225			TBX	FGRc08647		3.6E-42	
26054 ENU09849 ANI6IC1033 5:20012270	ANI61C1033 5:20012270			TBX	AFUc11528		6E-153	
26055 ENU09850 ANI61C1106 5:19763091	ANI61C1106 5:19763091			TBX	AFUc12698		1.3E-138	
26056 ENU09851 ANI61C1033 8:6521062	ANI61C1033 8:6521062			TBX	AFUc15802		5.7E-81	
26057 ENU09852 ANI61C1034 3:382104	ANI61C1034 3:382104			TBX	AFUc15194		1.2E-194	
26058 ENU09853 ANI61C1555: 14591665	ANI61C1555: 14591665			TBX	AFUc09094		2.2E-48	
26059 ENU09854 ANI61S1393: 3350	ANI61S1393: 3350			TBX	AFUc11981		8.7E-34	

## occupation of the contract of

Blast	re Prob % id cvrg Description "1.4e-96, 1.1e-16"	4.8E-39	6.6E-38	1.6E-71	7.4E-36	2.7E-142	5.5E-39	1.5E-150	1.2E-56	"3.7e-16, 1.1e-57"	1.9E-60	1.7E-49	3.3E-38	"1.1e-67, 1.3e-34, 3.5e-29"
aat Blast	Score Score													
u	Database Hit ncbi gi "AFUc10516, AFUc13253"	AFUc21007	AFUc15972	AFUc03100	AFUc05803	AFUc13299	AFUc15643	AFUc13299	AFUc13178	"AFUc04105, FGRc12288"	AFUc02462	AFUc11594	AFUc15700	"AFUc04942, AFUc11941, CALc04450"
Selection	Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer	3 pos													
Primer	5 pos									. <b>v</b>	-			7
	Contig source ANI61C1035 7:29371118	ANI61C1035 8:24522676	ANI61S1397: 31342	ANI61C1564. 10671316	ANI61C1036 0:12911680	ANI61C1036 0:33493570	ANI61C1036 0:3851	ANI61C1036 0:33163017	ANI61C1109 9:10511761	ANI61C1109 9:105671015	ANI61C403:	ANI61C1037 0:104925	, ANI61C1585 92490	3 ANJ61C410:
	num Seq id Contig source 26060 ENU09855 ANI61C1035 7:29371118	26061 ENU09856 ANI61C1035 8:24522676	26062 ENU09857 ANI61S1397: 31342	26063 ENU09858 ANI61C1564: 10671316	26064 ENU09859 ANI61C1036 0:12911680	26065 ENU09860 ANI61C1036 0:33493570	26066 ENU09861 ANI61C1036 0:3851	26067 ENU09862 ANI61C1036 0:33163017	26068 ENU09863 ANI61C1109 9:10511761	26069 ENU09864 ANI61C1109 9:105671015 4	26070 ENU09865 ANI61C403:1 2181006	26071 ENU09866 ANI61C1037 0:104925	26072 ENU09867 ANI61C1585: 92490	26073 ENU09868 ANI61C410:7 7388487
Sea	num 2606	26(	26(	26(	26(	26(	26(	26	26	26	26	26	26	26

Blast Blast % Score Prob % id cvrg Description 3.7E-70	4.3E-57	4.3E-57	1E-42	1E-42	5.6E-58	6.4E-48	1.5E-38	1.3E-33	9E-80	1.8E-113	5.9e-57	5.9e-75	2.7e-59
aat Database Hit ncbi gi Score AFUc05418	AFUc11022	AFUc11022	AFUc10295	AFUc10295	AFUc15010	AFUc02879	AFUc15422	AFUc03600	CALc05879	AFUc12803	Y13139	137	256
r Selection Basis TBX	TBX AFU	TBX AFU	TBX AFU	TBX AFU	TBX AFU	TBX AFU	TBX AFU	TBX AFU	TBX CAI	TBX AFC	TBX Y13	TBX Y13137	TBX Z71256
Primer Primer rice 5 pos 3 pos (2:1	12:6	12:7	1038 945	.038 298	038	593:	125:5	131:3	33:3	004: 5	145:2	028:	033:
Seq num Seq id Contig source 26074 ENU09869 ANI61C412:1 4401774	26075 ENU09870 ANI61C41 5236927	26076 ENU09871 ANI61C412:7 0087352	26077 ENU09872 ANIGIC1038 6:16311945	26078 ENU09873 ANI61C1038 6:19452298	26079 ENU09874 ANI61C10	26080 ENU09875 ANI61C15 241771	26081 ENU09876 ANI61C42 2095	26082 ENU09877 ANI61C43	26083 ENU09878 ANI61C433:3 5113186	26084 ENU09879 ANI61C8004: 22471915	26085 ENU09880 ANI61C4 3278	26086 ENU09881 ANI61C8028: 4092	26087 ENU09882 ANI61C8033: 60272

% id cvrg Description													
Blast Prob 2.7E-59	1.5E-44	7E-49	1.3E-32	5.6E-45	3E-62	1.2e-82	2E-57	1.1E-68	3E-39	1.2E-142	4.9E-55	8.8E-31	1.2E-53
aat Blast Score Score													
ncbi gi													
Database Hit AFUc12240	FGRc01319	AFUc11246	AFUc11373	AFUc14011	CALc04459	Z71256	AFUc14405	AFUc09357	AFUc15784	AFUc15221	CALc06130	AFUc15749	AFUc17865
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq id Contig source ENU09883 ANI61C7309: 5483	ANI61C7317: 22021795	ANI61C7317: 25792337	ANI61C7318: 19431584	ANI61C481:8 0589	ANI61C8051: 469212	ANI61C8051: 60745853	ANI61C8053: 22642734	ANI61C499:7 22455	ANI61C7331: 45994327	ANI61C6614: 16291394	ANI61C6621: 16001818	ANI61C8084: 31623470	ANI61C8085: 96612
Seq num Seq id 26088 ENU09883	26089 ENU09884 ANI61C7317: 22021795	26090 ENU09885 ANI61C7317: 25792337	26091 ENU09886 ANI61C7318: 19431584	26092 ENU09887 ANI61C481:8 0589	26093 ENU09888 ANIGIC8051: 469212	26094 ENU09889 ANI61C8051: 60745853	26095 ENU09890 ANI61C8053: 22642734	26096 ENU09891 ANI61C499:7 22455	26097 ENU09892 ANIGLC7331: 45994327	26098 ENU09893 ANI61C6614: 16291394	26099 ENU09894 ANI61C6621: 16001818	26100 ENU09895 ANI61C8084: 31623470	26101 ENU09896 ANI61C8085: 96612

aat Blast Blast % Score Score Prob % id cvrg Description 7.6E-172	4.4E-32	5.4E-64	1.5E-42	1.3E-36	4.4E-98	2.5E-63	"3.5e-64, 1.9e-59"	4.1E-44	8.3E-43	2.1E-47	2.7E-65	1.8E-32	"2.6e-39, 1.1e-16"
n Database Hit ncbi gi AFUc14910	AFUc12758	AFUc06255	AFUc05380	AFUc14011	AFUc15344	AFUc10645	"AFUc08731, FGRc07479"	AFUc08889	AFUc05668	AFUc12033	AFUc00567	FGRc11859	"AFUc04034, FGRc16556"
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26102 ENU09897 ANI61C7356: 26235	26103 ENU09898 ANI61C8087: 7711	26104 ENU09899 ANI61C6632: 431192	26105 ENU09900 ANI61C7365: 80097809	26106 ENU09901 ANI61C5911: 15631063	26107 ENU09902 ANI61C6644: 572294	26108 ENU09903 ANI61C7394: 15801083	26109 ENU09904 ANI61C7396: 65557882	26110 ENU09905 ANI61C6667: 23310	26111 ENU09906 ANI61C5941: 871323	26112 ENU09907 ANI61C6677: 39521	26113 ENU09908 ANI61C5957: 429757	26114 ENU09909 ANI61C5967: 90759284	26115 ENU09910 ANI61S2104: 5507

aat Blast Blast % ncbi gi Score Score Prob % id cvrg Description 1.2E-61	2.1E-49	1.3E-33	"7.6e-22, 1.9e-35"	3.1E-32	1E-32	2.9E-41	7.2E-40	3.4E-81	"1.3e-14, 4.3e-61"	2.5E-94	5.2E-57	4E-40	3.2E-48
Database Hit AFUc03602	AFUc15002	AFUc10036	"AFUc15479, AFUc21770"	AFUc11158	AFUc22275	AFUc14504	AFUc09171	AFUc11776	"AFUc10340, CALc05472"	AFUc07103	AFUc02776	AFUc21395	AFUc15972
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer Contig source 5 pos 3 pos ANI61C5978:	ANI61C3001: 4112	ANI61C5997: 990478	ANI61C3026: 56811	ANI61C2305: 1105612	ANI61C1110 7:652155	ANI61C1110 7:86868456	ANI61C3046: 869252	ANI61C2324: 416628	ANI61C3056: 33822980	ANI61C3062: 983432	ANI61C2334: 7641012	ANI61C1113 3:47644195	NI61C1040
Seq num Seq id Co 26116 ENU09911 AN	26117 ENU09912 ANI61C3001: 4112	26118 ENU09913 ANI61C5997: 990478	26119 ENU09914 ANI61C3026: 56811	26120 ENU09915 ANI61C2305: 1105612	26121 ENU09916 ANI61C1 7:65215	26122 ENU09917 ANI61C1 7:86868	26123 ENU09918 ANI61C3046: 869252	26124 ENU09919 ANI61C2324: 416628	26125 ENU09920 ANI61C3056: 33822980	26126 ENU09921 ANI61C3062: 983432	26127 ENU09922 ANI61C2334: 7641012	26128 ENU09923 ANI61CI 3:47644	26129 ENU09924 ANI61C1040

% % id cvrg Description												<b></b>	
Blast Prob 9.6E-52	5.4E-56	3.2E-107	2.3E-33	2.1E-56	5.9E-31	"5.9e-31, 2.6e-46"	6.8E-64	1.5E-68	2.7E-34	3.3E-55	"3.1e-53 8.7e-50"	7.7E-153	"4.0e- 150, 7.7e- 153"
Blast													
aat Score													
ncbi gi													
Database Hit AFUc07733	AFUc13075	AFUc13895	AFUc13910	AFUc05827	AFUc03564	"AFUc03564, AFUc19776"	AFUc03276	AFUc14564	AFUc12712	AFUc15740	"AFUc13557, X59720"	AFUc15804	"AFUc15804, AFUc15804"
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 26144 ENU09939 ANI61C1118 3:5814	26145 ENU09940 ANI61C1045 5:18312178	ANI61C1118 5:31412914	26147 ENU09942 ANIGICI118 6:22011884	ANI61C1118 9:8801347	26149 ENU09944 ANI61C1668: 9611218	26150 ENU09945 ANIGIC1668: 14232232	26151 ENU09946 ANIGIC1119 3:724206	ANI61C1046 4:16517	26153 ENU09948 ANI61C508:2 8332485	ANI61C1047 7:77668083	26155 ENU09950 ANI61C1047 7:108451121	ANI61C1048 3:19062700	26157 ENU09952 ANI61C1048 3:32783486
Seq id 4 ENU09939	5 ENU09940	26146 ENU09941 ANI61C1 5:31412	7 ENU09942	26148 ENU09943 ANI61C1 9:88013	9 ENU09944	0 ENU09945	1 ENU09946	26152 ENU09947 ANI61C1 4:16517	3 ENU09948	26154 ENU09949 ANI61C1 7:77668	5 ENU09950	26156 ENU09951	7 ENU09952
Seq num 26144	2614:	26140	2614′	2614	26149	2615	2615	2615	2615.	2615	2615	2615	2615

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26158 ENU09953 ANI61C1048 3:999763 3:999763 3:999763 3:999763 3:999763 3:999763 3:999763 4.69328598 7:69328598 43203898 43203898 43203898 56830 56830 7:63127257 7:63127257 26164 ENU09959 ANI61C530:6 2595831 26165 ENU09960 ANI61C534:7 9587584 26166 ENU09961 ANI61C539:7 8097	Selection Basis TBX TBX TBX TBX TBX TBX TBX TBX		aat Blast Blast Score Score Prob 5.2E-89 5.2E-89 9.8e-121" 3.6E-38 3.5E-63 7.54e-36, 1.8e-70" 4.6e-17 4.6e-17 4.6e-17 1.9E-69	% id cvrg Description 89 % id cvrg Description -25, 63 63 -36, 70" 17
26167 ENU09962 ANI61C8115: 151157 26168 ENU09963 ANI61C8119: 1234920 26169 ENU09964 ANI61C556:5 6475390 26170 ENU09965 ANI61C558:4 3204880 26171 ENU09966 ANI61C562:3 1312799	X8T X8T X8T X8T X8T X8T	AFUc15481 AFUc08845 AFUc14924 AFUc14136 AFUc06316	4.6E-151 1.7E-82 1.1E-218 3E-62 5.9E-41	4.6E-151 1.7E-82 1.1E-218 3E-62 5.9E-41

## nounced near near

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26172 ENU09967 ANI61C8133:	Selection Basis TBX	Database Hit ncbi gi AFUc11118		% id cvrg Description
26173 ENU09968 ANI61C578:5 771029	TBX	AFUc01862	3.6E-64	
26174 ENU09969 ANI61C8140: 93864	TBX	"AFUc00985, AFUc03101"	"1.7e-16, 6.6e-43"	
26175 ENU09970 ANI61C7419: 511140	TBX	AFUc15103	2.7E-52	
26176 ENU09971 ANI61C7419: 1006668	TBX	AFUc15103	2.7E-52	
26177 ENU09972 ANI61C8155: 2232	TBX	AFUc15172	2.4E-43	
26178 ENU09973 ANI61C592:4 591	TBX	FGRc12433	5.6E-42	
26179 ENU09974 ANI61C7430: 12501047	TBX	AFUc05191	3.2E-97	
26180 ENU09975 ANI61C6703: 8471110	TBX	AFUc14632	7.8E-86	
26181 ENU09976 ANI61C6703: 23161740	TBX	AFUc14632	3.3E-72	
26182 ENU09977 ANI61C6709: 40014468	TBX	AFUc03350	2.4E-52	
26183 ENU09978 ANI61C6711: 20591173	TBX	AFUc14433	2.9E-154	
26184 ENU09979 ANI61C6711: 27722153	TBX	AFUc14433	2.9E-154	
26185 ENU09980 ANI61C6714: 61746386	TBX	AFUc14412	4.5E-35	

Blast Blast % e Score Prob % id cvrg Description 2.8e-34	5.7E-52	2E-44	2.8E-136	5.2E-35	1E-93	1.4E-59	5E-78	2.3E-31	9.5E-73	8.6E-45	1.8E-60	4.4E-55	1.1e-95
on Database Hit ncbi gi Score Y13138	AFUc14993	AFUc04684	AFUc14734	AFUc13156	AFUc08563	AFUc02841	AFUc13631	AFUc11189	AFUc11182	AFUc01472	AFUc18290	AFUc12936	Y13134
Primer Primer Selection 5 pos 3 pos Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq num Seq id Contig source 5 pos 26186 ENU09981 ANI61C6717: 16671895	26187 ENU09982 ANI61C7455: 28012121	26188 ENU09983 ANI61C6728: 254499	26189 ENU09984 ANI61C7465: 74283	26190 ENU09985 ANI61C7485: 30343324	26191 ENU09986 ANI61C7492: 14599	26192 ENU09987 ANI61C6764: 431997	26193 ENU09988 ANI61C6772: 18851670	26194 ENU09989 ANI61C6772: 33662850	26195 ENU09990 ANI61C6777: 17392320	26196 ENU09991 ANI61C6779. 885.415	26197 ENU09992 ANI61C6785: 400657	26198 ENU09993 ANI61S2209: 58463	26199 ENU09994 ANI61C3104: 37333464

Seq num Seq id 26200 ENU09995	Contig source ANI61C3122: 355765	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc15397	aat Blast i Score Score	Blast Prob 3.3E-72	% id cvrg Description
26201 ENU09996 ANI61C2410: 11111348	ANI61C2410: 11111348			TBX	AFUc10475		9E-39	
26202 ENU09997 ANI61C2410: 18412470	ANI61C2410: 18412470			TBX	"AFUc14120, AFUc14120"		"1.3e- 116, 1 8e-98"	
26203 ENU09998	ANI61C1121 7:4291			TBX	CALc01737		5.9E-34	
26204 ENU09999 ANI61C3151: 7661116	ANI61C3151: 7661116			TBX	AFUc12817		1.4E-34	
26205 ENU10000 ANI61C1122 5:2694	ANT61C1122 5:2694			TBX	AFUc11815		3.1E-62	
26206 ENU10001 ANI61C1122 5:8791377	ANI61C1122 5:8791377			TBX	"AFUc11815, AFUc11815"		"2.4e-54, 3.1e-62"	
26207 ENU10002 ANI61C1122 9:36712959	ANT61C1122 9:36712959			TBX	AFUc15733		1.7E-120	
26208 ENU10003 ANI61C1700: 23397	ANI61C1700: 23397			TBX	AFUc13133		3.5E-35	
26209 ENU10004 ANI61C1701: 20762837	ANI61C1701: 20762837			TBX	AFUc15352		1.3E-62	
26210 ENU10005 ANI61C1705: 33993761	33993761			TBX	AFUc08134		1.8E-44	
26211 ENU10006 ANI61C2436: 9571347	5 ANI61C2436: 9571347			TBX	AFUc15614		2.4E-85	
26212 ENU10007 ANI61C1123 4:4673	7 ANI61C1123 4:4673			TBX	AFUc15455		2.2E-40	
26213 ENU10008 ANI61C1124 0:2461	3 ANI61C1124 0:2461			TBX	AFUc06703		9.7E-46	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26214 ENU10009 ANI61C3182: 20312377	Selection Basis TBX	Database Hit ncbi gi AFUc04772	aat Blast Blast Score Score Prob 7E-47	% % id cvrg Description
26215 ENU10010 ANI61C3185: 508145	TBX	AFUc13049	1.7E-126	
26216 ENU10011 ANI61C3186: 31062741	TBX	AFUc13434	7.6E-45	
26217 ENU10012 ANI61C1730: 3527	TBX	AFUc10266	6.5E-59	
26218 ENU10013 ANI61C3191: 2783	TBX	AFUc15545	3.8E-87	
26219 ENU10014 ANI61C2464: 16681021	TBX	FGRc11747	1.2E-31	
26220 ENU10015 ANI61C3199: 1611	TBX	AFUc15519	1.3E-45	
26221 ENU10016 ANI61C1741: 61833	TBX	AFUc15826	8.6E-41	
26222 ENU10017 ANI61C2473:	TBX	"AFUc09645, AFUc09645"	"3.3e-31, 7.9e-54"	
26223 ENU10018 ANI61C1054 1:29332106	TBX	"AFUc12046, Y13140"	"6.8e-95, 3.0e- 130"	
26224 ENU10019 ANI61C1127 4:1813796	TBX	"FGRc06649, FGRc11623"	"3.8e-34, 9.9e-11"	
26225 ENU10020 ANI61C1127 9:17250	TBX	AFUc07741	8.7E-61	
26226 ENU10021 ANI61C2480: 240440	TBX	AFUc08744	6.3E-48	
26227 ENU10022 ANI61C1759: 1431460	TBX	"AFUc11420, AFUc18306"	"3.8e-51, 2.0e-21"	

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Blast Blast % Score Prob % id cvrg Description 8.7E-101	8.4E-74	6.9E-52	2.3E-76	1.5E-72	1.2E-65	"1.3e-12, 1.3e-51, 1.0e-33"	2.5E-83	1.1E-67	2.9E-38	3.3E-98	9.4E-32	1.0e-18	1.2E-64
aat Score													
t ncbi gi						., 6,							
Database Hit CALc06110	AFUc05645	AFUc13557	AFUc14306	CALc06158	AFUc13158	"AFUc00606, AFUc06517, FGRc10385"	AFUc03864	AFUc14174	AFUc14725	AFUc13200	AFUc07883	Y13136	AFUc07639
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 26228 ENU10023 ANI61C1055 3:21320	26229 ENU10024 ANI61C1055 5:26991999	26230 ENU10025 ANI61C1055 7:46796	26231 ENU10026 ANI61C2495: 5213	26232 ENU10027 ANI61C600:2 1741764	26233 ENU10028 ANI61C602:9 74355	26234 ENU10029 ANI61C1057 2:571135	26235 ENU10030 ANI61C1057 3:10241449	26236 ENU10031 ANI61C613:3 584	26237 ENU10032 ANI61C1058 2:54572	26238 ENU10033 ANI61C1058 9:79288383	26239 ENU10034 ANI61C1059 2:24262656	26240 ENU10035 ANI61C634:8 86629	26241 ENU10036 ANI61C656:3 4618

Seq num Seq id Contig source 26242 ENU10037 ANI61C669:3 2348		Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc11626	aat Score	Blast	Blast Prob 1.7E-36	% % id cvrg Description	
26243 ENU10038 ANI61C8230: 165455	ANI61C8230: 165455			TBX	FGRc11456			1.9E-37		
26244 ENU10039 ANI61C7508: 1555372	ANI61C7508: 1555372			TBX	AFUc09787			6.4E-78		
26245 ENU10040 ANI61C671:4 82808	ANI61C671:4 82808			TBX	AFUc15558			4.8E-61		
26246 ENU10041 ANI61C686:4 6955262	ANI61C686:4 6955262			TBX	AFUc13870			7.5E-43		
26247 ENU10042 ANIGLC7523: 17902362	ANI61C7523: 17902362			TBX	AFUc06950			1.4E-52		
26248 ENU10043 ANI61C7528: 3953	ANI61C7528: 3953			TBX	AFUc15740			1.2E-39		
26249 ENU10044 ANI61C699:3 532	ANI61C699:3 532			TBX	AFUc09402			3.2E-44		
26250 ENU10045 ANI61C7530: 972442	ANI61C7530: 972442			TBX	AFUc11771			2.1E-55		
26251 ENU10046 ANI61C7531: 27793147	ANI61C7531: 27793147			TBX	CALc05550			1.4E-32		
26252 ENU10047 ANI61C7535: 5481081	ANI61C7535: 5481081			TBX	AFUc15071			2.3E-118		
26253 ENU10048 ANI61C7535: 3803	ANI61C7535: 3803			TBX	AFUc13442			4.5E-43		
26254 ENU10049 ANI61C6808: 21622704	ANI61C6808: 21622704			TBX	AFUc13976			5.2E-32		

% id cvrg Description												
Blast Blast Score Prob % id "1.8e- 113, 5.7e-40, 2.6e-74, 3.5e-13"	1.8E-170	7.4E-91	5.2E-32	1.5e-69	1.9E-86	"1.9e-86, 5.6e-26"	3.4E-57	9.6E-34	3.6E-33	4.3E-66	2.6E-33	2.1E-45
aat Score												
Database Hit ncbi gi "AFUc06527, AFUc17241, FGRc09005,	FGRc12425	AFUc11234	AFUc04450	Y13140	AFUc14565	"AFUc14565, AFUc14565"	AFUc08494	AFUc15969	AFUc14056	AFUc11416	AFUc13638	AFUc15186
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos												
Primer 5 pos												
Seq num Seq id Contig source 26255 ENU10050 ANI61C6814: 34231721	26256 ENU10051 ANIGIC8273: 14041688	26257 ENU10052 ANI61C8273: 38733640	26258 ENU10053 ANI61C8273: 49194605	26259 ENU10054 ANI61C7546: 5699	26260 ENU10055 ANI61C6819: 36061	26261 ENU10056 ANI61C6819: 1172511	26262 ENU10057 ANI61C6823: 47586	26263 ENU10058 ANIGIC6827: 1241709	26264 ENU10059 ANIGIC7560: 710153	26265 ENU10060 ANI61C8293: 17361422	26266 ENU10061 ANI61C6867: 41994710	26267 ENU10062 ANI61C6875: 487.239

### outuan center

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26268 ENU10063 ANI61C6880: 4226	Selection Basis TBX	Database Hit ncbi gi AFUc09175	aat Blast Blast Score Score Prob 3.8E-41	% % id cvrg Description
26269 ENU10064 ANI61C6892: 286771	TBX	AFUc01364	1.2E-43	
26270 ENU10065 ANI61C6895: 48635	TBX	AFUc20237	3.8E-48	
26271 ENU10066 ANI61C3208: 20182563	TBX	AFUc10936	5.8E-66	
26272 ENU10067 ANI61S3046: 93596	TBX	AFUc15363	4.9E-51	
26273 ENU10068 ANI61C3229: 25332303	TBX	AFUc08535	1.3E-33	
26274 ENU10069 ANI61C2509: 32782802	TBX	AFUc14181	8.3E-66	
26275 ENU10070 ANI61C3241: 14821832	TBX	AFUc11766	4.3E-36	
26276 ENU10071 ANI61C1131 1:12691808	TBX	AFUc07214	9.1E-36	
26277 ENU10072 ANI61C3253: 12382259	TBX	AFUc15072	7.1E-105	
26278 ENU10073 ANIGIC1132 1:15172423	TBX	AFUc10674	3.3E-98	
26279 ENU10074 ANI61S1636: 3353	TBX	AFUc02091	6.5E-41	
26280 ENU10075 ANI61C2549: 36604	TBX	FGRc12323	5.1E-35	
26281 ENU10076 ANI61C1134 1:37223447	TBX	CALc05684	4.8E-52	

aat Blast Blast % Score Score Prob % id cvrg Description 5.9E-35	2.6E-44	5.7E-58	5.6E-35	3.2E-42	2.7e-20	9.9E-61	2.1E-33	2.3E-64	2E-37	3.8E-37	1.9E-70	1.9E-70	3.6E-101
n Database Hit ncbi gi AFUc10087	AFUc05589	AFUc04288	AFUc09584	AFUc15619	Z71256	AFUc15114	FGRc10919	AFUc13573	AFUc01485	AFUc09670	AFUc10676	AFUc10676	AFUc15969
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26282 ENU10077 ANI61S1654:	26283 ENU10078 ANI61C2553: 14374	26284 ENU10079 ANIGIC2553: 25273117	26285 ENU10080 ANI61C1062 4:26702122	26286 ENU10081 ANI61C1135 7:34367	26287 ENU10082 ANI61C1836: 5167	26288 ENU10083 ANI61C3299: 7721486	26289 ENU10084 ANI61C1063 4:3416	26290 ENUI0085 ANI61C1136 3:2495	26291 ENU10086 ANI61S1673: 438133	26292 ENU10087 ANI61C1840: 50642	26293 ENU10088 ANI61C1064 6:757247	26294 ENU10089 ANI61C1064 6:13791034	26295 ENU10090 ANI61C1850: 10151

Blast I	1.0c-00 2.1E-47	1.8E-51	3.8E-61	"1.4e- 160, 4.5e- 167"	4.5E-167	4.5E-167	5.4E-33	2E-118	3.1E-34	2.3E-50	5.1E-41	2.2E-85	9.9E-50
Database Hit ncbi gi "AFUc15290, FGRc03192"	AFUc04784	AFUc07894	AFUc14134	"AFUc15965, AFUc15965"	AFUc15965	AFUc15965	AFUc19996	AFUc15856	AFUc01385	AFUc02664	AFUc11950	AFUc13744	AFUc12305
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 26296 ENU10091 ANI61C1065 4:56286366	26297 ENU10092 ANI61C1138 4:961456	26298 ENU10093 ANI61C1138 6:949477	26299 ENU10094 ANI61C2598: 16491030	26300 ENU10095 ANI61C1139 3:10621801	26301 ENU10096 ANI61C1139 3:27173327	26302 ENU10097 ANI61C1139 3:34544047	26303 ENU10098 ANI61C1139 8:14071883	26304 ENU10099 ANI61C1066 9:26502192	26305 ENU10100 ANI61C1871: 642304	26306 ENU10101 ANI61C702:9 296	26307 ENU10102 ANI61C1067 0:2412	26308 ENUI0103 ANI61C9007: 3904.4113	26309 ENU10104 ANI61C1886:

# وويد كالبابي كالمادي كالمادي

aat Blast Blast % Score Score Prob % id cvrg Description 1.5E-45	5.9e-45	2.1e-120	1.2E-43	9.5E-47	2.4E-73	4.1E-34	2.2E-42	4.3E-51	9.8E-39	6E-94	1.3E-216	7.7E-116	"5.1e-41, 1.7e-14"
on Database Hit ncbi gi AFUc16162	X59720	Y13134	AFUc01808	AFUc15403	AFUc10157	FGRc08015	AFUc04230	AFUc15972	AFUc01794	AFUc07695	AFUc15782	AFUc15173	"AFUc09562, AFUc16430"
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26310 ENU10105 ANI61C1068 6:674357	26311 ENU10106 ANI61C1899: 1216	26312 ENU10107 ANI61C722:3 5403286	26313 ENU10108 ANI61C1069 1:232450	26314 ENU10109 ANI61C1069 2:18662621	26315 ENU10110 ANI61C9024: 3342	26316 ENU10111 ANI61C736:4 557	26317 ENU10112 ANI61C742:9 861309	26318 ENUI0113 ANI61C9041: 769225	26319 ENU10114 ANI61C8314: 8471149	26320 ENU10115 ANI61C754:1 6942598	26321 ENU10116 ANI61C759:9 741656	26322 ENU10117 ANI61C760:8 241195	26323 ENU10118 ANI61C9060: 4891082

#### nough concern

Seq num Seq id Contig 26324 ENU10119 ANIG10	source C7602:	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc08499	aat Blast Score Score	Blast Prob 2E-43	% % id cvrg Description
26325 ENU10120 ANI61C7611: 26618	1 1C7611: 18			TBX	AFUc01029		1E-34	
26326 ENU10121 ANI61C9078: 1169627	.627			TBX	"CALc05486, Y13140"		"1.7e- 172, 9.9e-	
26327 ENU10122 ANI61C9081: 2544	1C9081:			TBX	AFUc09562		18/" 3.3E-71	
26328 ENU10123 ANI61C796:2 0001580	ANI61C796:2 0001580			TBX	Z71256		1.1e-94	
26329 ENU10124 ANI61C797:3 0733285	1C797:3 3285			TBX	AFUc14002		2E-68	
26330 ENUI0125 ANI61C6901: 3691157	ANI61C6901: 3691157			TBX	AFUc11697		1.6E-66	
26331 ENU10126 ANI61C6908: 2382	1C6908: 2			TBX	AFUc11236		2E-80	
26332 ENU10127 ANI61C8372: 68310	1C8372: 10			TBX	FGRc10332		2.9E-38	
26333 ENU10128 ANI61C6936: 11451738	ANI61C6936: 11451738			TBX	AFUc00849		5.3E-50	
26334 ENUI0129 ANI61C6941: 1300322	1C6941: 322			TBX	AFUc13344		4.8E-76	
26335 ENU10130 ANI61C7675: 15071737	51C7675: 1737			TBX	AFUc15563		2.7E-84	
26336 ENU10131 ANI61S617:5 00105	51S617:5 05			TBX	AFUc05623		7E-47	
26337 ENU10132 ANI61C24:48 2219	51C24:48 9			TBX	AFUc10888		2.2E-38	

Blast % Prob % id cvrg Description 3E-62	4.7E-59	1E-47	4.5E-34	8.8E-42	5.9E-36	3.8E-40	2E-50	1.9E-71	3.8E-51	5.4E-37	5.6E-52	1.4E-40	2.4E-38
aat Blast ncbi gi Score Score													
Database Hit AFUc03140	AFUc10817	AFUc14695	AFUc11715	AFUc10584	AFUc13720	FGRc12892	FGRc10359	AFUc11668	AFUc06769	AFUc07689	FGRc02814	FGRc10078	AFUc13163
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 5 26338 ENU10133 ANI61C24:39 123514	26339 ENU10134 ANI61C4002: 20091581	26340 ENU10135 ANI61C6983: 9611700	26341 ENU10136 ANI61C4013: 122460	26342 ENU10137 ANI61C6992: 26123298	26343 ENU10138 ANI61C4029: 80709	26344 ENU10139 ANI61C4034: 851537	26345 ENU10140 ANI61C74:24 011973	26346 ENU10141 ANI61C80:31 133924	26347 ENU10142 ANI61C82:17 261385	26348 ENU10143 ANI61C4062: 7451218	26349 ENU10144 ANI61C95:21 131149	26350 ENU10145 ANI61C96:15 171230	26351 ENU10146 ANI61C1140 1:3434

% % id cvrg Description													
Blast Prob 2.6E-35	5.8E-31	2E-44	5.5E-42	6.5E-148	2.1E-47	"1.4e-62, 1.4e-35"	2.4E-82	9.7E-36	"2.2e-40, 6.0e-31"	3.4E-32	6.5E-95	1.4E-103	1.2E-40
aat Blast Score Score													
ncbi gi													
Database Hit AFUc12822	AFUc13641	AFUc18684	AFUc13016	AFUc13919	AFUc09698	"FGRc04985, Y13140"	AFUc06488	AFUc19770	"AFUc17439, AFUc17439"	AFUc10345	AFUc15684	AFUc14697	AFUc21889
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer 5 pos 3 pos													
Contig source ANI61C1072 5:52816	ANI61C2662: 25512306	ANI61C3398: 387870	ANI61C1146 2:38294053	ANI61C2676: 3305	ANI61C2679: 1222893	ANI61C1954: 6799	ANI61C2684: 71694	ANI61C1075 3:1340981	3:17231472	ANI61C1076 2:980528	ANI61C805:2 2332634	ANI61C1077 1:216.4	. ANI61C1077 6:38384329
Seq num Seq id 26366 ENU10161	26367 ENU10162 ANI61C2662: 25512306	26368 ENU10163 ANI61C3398: 387870	26369 ENUI0164 ANI61C1146 2:38294053	26370 ENU10165 ANI61C2676: 3305	26371 ENU10166 ANI61C2679: 1222893	26372 ENU10167 ANI61C1954: 6799	26373 ENU10168 ANI61C2684: 71694	26374 ENU10169 ANI61C1075 3:1340981	26375 ENUI0170 ANIGICI075 3:17231472	26376 ENUI0171 ANI61C1076 2:980528	26377 ENU10172 ANI61C805:2 2332634	26378 ENUI0173 ANI61CI0 1:2164	26379 ENU10174 ANIGIC1077 6:38384329

## ofest statement

aat Blast Blast % Score Score Prob % id cvrg Description 7.3E-40	8.6E-33	3.6E-62	2E-48	4.2E-73	7.SE-55	1.4E-64	7.1E-84	1.5E-63	3.7E-51	3.1E-55	1.5E-50	1.2E-34	"1.4e-27, 2.5e-41"
n Database Hit ncbi gi AFUc01187	CALc05989	AFUc14184	AFUc08719	AFUc12106	AFUc15553	AFUc13583	CALc05289	AFUc10565	AFUc00801	AFUc01270	AFUc15449	AFUc13368	"AFUc16323, Y13140"
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26380 ENU10175 ANI61C9104: 5284	26381 ENU10176 ANI61C810:2 052	26382 ENU10177 ANI61C1078 4:34723786	26383 ENU10178 ANI61C9110: 222683	26384 ENUI0179 ANI61C9112: 71196715	26385 ENU10180 ANI61C1990: 33308	26386 ENU10181 ANI61C8403: 4752	26387 ENU10182 ANI61C9135: 16691460	26388 ENU10183 ANI61C843:2 5392069	26389 ENU10184 ANI61C847:4 82111	26390 ENU10185 ANI61C9142: 131346	26391 ENU10186 ANI61C854:6 191	26392 ENU10187 ANI61C8426: 3891	26393 ENU10188 ANI61C861:3 675

aat Blast Blast % Score Score Prob % id cvrg Description 4.9E-32	2.3E-64	3.3E-33	7.3E-33	7E-61	1.6E-40	4.1E-49	1.2E-37	"2.2e-54, 7.4e-41, 2.3e-26, 1.7e-34"	2.5E-129	3E-104	1.1E-84	5.3E-40	3.6E-35
Database Hit ncbi gi AFUc14973	AFUc12089	FGRc09602	FGRc18440	AFUc05401	AFUc14668	AFUc08030	AFUc14112	"AFUc09443, AFUc09443, FGRc19689, 1100093"	AFUc15223	AFUc10030	AFUc14162	AFUc12028	AFUc15553
ner Selection os Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26394 ENU10189 ANI61C9162:	26395 ENU10190 ANI61C7710: 77535	26396 ENU10191 ANI61C7715: 39174234	26397 ENU10192 ANI61C7717: 64286108	26398 ENU10193 ANI61C880:1 600692	26399 ENU10194 ANI61C8450: 20301656	26400 ENU10195 ANI61C9184: 31390	26401 ENU10196 ANI61C7728: 1528953	26402 ENU10197 ANI61C8457: 63145572	26403 ENU10198 ANI61C8459: 20321801	26404 ENU10199 ANI61C8459: 90648759	26405 ENUI0200 ANI6IC893:2 4012670	26406 ENU10201 ANI61C7735: 7541065	26407 ENUI0202 ANI61C8480: 888511

## becelo osnich

aat Blast Blast % Score Score Prob % id cvrg Description 5.4E-77	5E-90	6.9E-138	1.6E-33	7.8E-46	4.4E-40	1.1E-40	2.2E-72	3E-38	2.3E-66	"9,4e- 22"	1.1E-35	1.6E-95	9.6E-40
n Database Hit ncbi gi CALc04830	AFUc14523	AFUc05805	AFUc10213	AFUc01898	AFUc09951	FGRc11175	AFUc15131	AFUc15554	AFUc08075	U00094	AFUc01742	FGRc07284	AFUc12614
r Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26408 ENU10203 ANI61C8486:	26409 ENU10204 ANI61C8494: 34772449	26410 ENU10205 ANI61C7767: 16522095	26411 ENU10206 ANI61C7776: 16431987	26412 ENU10207 ANI61S710:8 8441	26413 ENU10208 ANI61S34:6 293	26414 ENU10209 ANI61S42:40 923	26415 ENU10210 ANI61C4105: 15.279	26416 ENU10211 ANT61C4108: 4323	26417 ENU10212 ANI61C3402: 16781353	26418 ENU10213 ANI61C4132: 581807	26419 ENU10214 ANI61C4132: 11381458	26420 ENU10215 ANI61C4132: 32403479	26421 ENU10216 ANI61C3412: 7111163

# chatain as anama

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26422 ENU10217 ANI61C4144:	Selection Basis TBX	Database Hit ncbi gi AFUc18185	aat Blast Blast Score Score Prob 3E-49	% id cvrg Description
26423 ENU10218 ANI61C4146: 2066	TBX	AFUc11980	2.7E-48	
26424 ENU10219 ANI61C3427: 23002070	TBX	AFUc11170	1.1E-32	
26425 ENU10220 ANI61C4157: 39873415	TBX	"AFUc22639, Y13135"	"1.5e-13, 3.2e-25"	
26426 ENU10221 ANI61C4160: 27296	TBX	AFUc20192	5.3E-35	
26427 ENU10222 ANI61C3443: 51224	TBX	AFUc17062	4.4E-47	
26428 ENU10223 ANI61C4182: 28423151	TBX	Y13136	2.5e-18	
26429 ENU10224 ANI61C4192: 40523765	TBX	AFUc14724	3.7E-90	
26430 ENU10225 ANI61C4194: 21502505	TBX	AFUc11112	1E-37	
26431 ENU10226 ANI61C4195: 8091015	TBX	AFUc11252	5.6E-91	
26432 ENU10227 ANI61C4199: 7941340	TBX	"AFUc01489, AFUc19265"	"9.5e-48, 7.7e-08"	
26433 ENU10228 ANI61C3474: 8533	TBX	AFUc06878	3.1E-82	
26434 ENU10229 ANI61S2581: 2439	TBX	"AFUc18278, CALc04638"	"1.3e-25, 1.3e-31"	
26435 ENU10230 ANI61C3481: 4245	TBX	AFUc10462	1.5E-38	

# occupation of the companies of the compa

aat Blast Blast % ncbi gi Score Score Prob % id cvrg Description 1.7E-68	5.8E-77	1.7E-54	4.5E-54	"6.4e-78, 1.6e-38"	7.2E-31	9.0e-47	2.2E-46	2.3E-79	5.5E-34	2.9E-66	1.8E-56	"3.1e-67, 9.1e-74"	9.6E-38
Database Hit AFUc14374	AFUc13692	AFUc14947	AFUc10042	"AFUc08795, AFUc08853"	AFUc04411	Z71256	CALc05922	FGRc11250	AFUc15937	AFUc14249	AFUc05949	"AFUc15972, AFUc15972"	FGRc10423
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer Contig source 5 pos 3 pos ANI61S1867:	161C2763: 02	161C2774: 4	ANI61C1084 9:32483499	ANI61C1085 5:21912922	ANI61C2798: 939448	ANI61C900:4 94760	ANI61C904:1 5331126	1161C9202: 01717	ANI61C1088 8:17671118	II61C9214: 54	II61C9214: :42441	ANI61C1089 0:821020	T61C1089
Seq num Seq id Cont 26436 ENU10231 ANI	26437 ENU10232 ANI61C2763: 8802	26438 ENU10233 ANI61C2774: 5254	26439 ENU10234 ANI61C1084 9:32483499	26440 ENU10235 ANI61C1085 5:21912922	26441 ENU10236 ANI61C2 939448	26442 ENU10237 ANI61C900:4 94760	26443 ENU10238 ANI61C904:1 5331126	26444 ENU10239 ANI61C9202: 20101717	26445 ENU10240 ANI61C1 8:17671	26446 ENU10241 ANI61C9214	26447 ENU10242 ANI61C9214: 28242441	26448 ENU10243 ANI61C1 0:82102	26449 ENUI0244 ANI61C1089

## states and the substitutions

Primer Primer Selection  Contig source 5 pos 3 pos Basis Database Hit ncbi gi Score Score Prob % id cvrg Description ANI61C9221: 2.7E-72	19822254 ANI61C936:1 TBX AFUc15330 2.4E-132	465.1980 ANIGIC8502: TBX "AFUc03429, "2.2e-09, AFT 12.18078" 0.72 43"	TBX AFUc13932	ANI61C945:2 TBX AFUc13932 8.5E-51 8542606	ANI61C8510: TBX AFUc14805 2.3E-52	ANI61C8529: TBX FGRc02575 1.3E-33	ANI61C8537: TBX FGRc10154 5.6E-44 10883	ANI61C9268: TBX AFUc20576 3.3E-49 45694189	ANI61C9269: TBX "AFUc14083, "1.9e-19, 17412743 AFUc15534" 5.3e-32"	ANI61C7811: TBX AFUc13321 1.9E-33	ANI61C9273: TBX AFUc05348 26E-34 2301	ANI61C9274: TBX AFUc10007 9.1E-49 13601106	
Seq Prir num Seq id Contig source 5 pc 26450 ENU10245 ANI61C9221:		4651980 26452 ENU10247 ANI61C8502:	26453 ENU10248 ANI61C945:2 6061959	26454 ENU10249 ANI61C945:2 8542606	26455 ENU10250 ANI61C8510: 22001793	26456 ENU10251 ANI61C8529: 15472065	26457 ENU10252 ANI61C8537: 108833	26458 ENU10253 ANI61C9268: 45694189	26459 ENU10254 ANI61C9269: 17412743	26460 ENU10255 ANI61C7811: 3528	26461 ENU10256 ANI61C9273: 2301	26462 ENU10257 ANI61C9274: 13601106	

# che e e e e e e e e e e e e e e

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26464 ENU10259 ANIG1C7821:		Database Hit ncbi gi AFUc13640	aat Blast Score Score	9	% id cvrg Description
26465 ENU10260 ANI61C8551: 12492174	TBX	AFUc12117		3E-62	
26466 ENU10261 ANI61C7825: 23871959	TBX	AFUc07632		2.4E-80	
26467 ENU10262 ANI61C7829: 128622	TBX	AFUc00937		2E-53	
26468 ENU10263 ANI61C9289: 2191253	TBX	AFUc10073		1.4E-40	
26469 ENU10264 ANI61C991:1 7562	TBX	AFUc14674		1.4E-69	
26470 ENU10265 ANI61C9294: 468671	TBX	AFUc10456		6E-31	
26471 ENU10266 ANI61C8565: 1585	TBX	AFUc03126		1.9E-62	
26472 ENU10267 ANI61C9295: 44063	TBX	AFUc08217		1.7E-83	
26473 ENU10268 ANI61C8570: 84278742	TBX	"FGRc03639, U00094"		"6.3e-39, 3.4e-49"	
26474 ENU10269 ANI61C8573: 55264607	TBX	"FGRc22681, FGRc23949"		"3.2e-16, 5.3e-58"	
26475 ENU10270 ANI61C8575: 12822046	TBX	AFUc00968		1.5E-62	
26476 ENU10271 ANI61C8580: 188637	TBX	AFUc07749		1.5E-57	
26477 ENU10272 ANI61C7851: 25212318	TBX	AFUc15780		1.2E-49	

# ceron ospina

aat Blast Blast % i gi Score Score Prob % id cvrg Description 9E-55	1.4E-76	"2.4e-51, 9.0e-51"	6.5E-44	"1.2e-34, 5.1e-39"	2.1E-42	7.6E-52	8.5e-18	5.5E-40	4.9E-32	5.5E-67	1.8E-56	2E-52	"2.1e-33, 3.4e-46"
Database Hit ncbi gi AFUc06805	AFUc12018	"AFUc00688, AFUc00688"	AFUc18887	"AFUc14236, AFUc14236"	AFUc15972	AFUc15269	Y13137	AFUc13855	FGRc11037	AFUc14037	AFUc08092	AFUc01021	"AFUc01646, AFUc11287"
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26478 ENU10273 ANI61C7865: 13511782	26479 ENU10274 ANI61C7870: 23952601	26480 ENU10275 ANI61C7885: 1235826	26481 ENU10276 ANI61C7896: 72566	26482 ENUI0277 ANI61S822:6 21386	26483 ENU10278 ANI61S3327: 45308	26484 ENU10279 ANI61C4225: 20911639	26485 ENU10280 ANI61C4226: 37513	26486 ENU10281 ANI61S853:4 2420	26487 ENU10282 ANI61C4239: 5962	26488 ENU10283 ANI61C4242: 32023477	26489 ENU10284 ANI61C4262: 113679	26490 ENU10285 ANI61C4263: 3776	26491 ENU10286 ANI61C2812: 3762

#### isto e e e is e company

Seq num Seq id 26492 ENU10287	Seq id Contig source ENU10287 ANI61C4270: 42424855	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc02593	aat Blast Score Score	Blast Prob 2.2E-34	% % id cvrg Description
26493 ENU10288 ANI61C3544: 35543094	ANI61C3544: 35543094			TBX	AFUc12369		1.4E-40	
26494 ENU10289 ANI61C2817: 37315	ANI61C2817: 37315			TBX	AFUc15017		1.3E-45	
26495 ENU10290 ANI61C3548: 14611129	ANI61C3548: 14611129			TBX	FGRc26479		2.3E-41	
26496 ENU10291 ANI61S1939: 606169	ANI61S1939: 606169			TBX	AFUc13323		3.7E-38	
26497 ENU10292 ANI61C3566: 42394448	ANI61C3566: 42394448			TBX	Y13136		1.4e-52	
26498 ENU10293 ANI61C1090 0:536907	ANI61C1090 0:536907			TBX	FGRc11747		9.5E-32	
26499 ENU10294 ANI61C3588: 22782856	ANI61C3588: 22782856			TBX	AFUc13885		2.5E-56	
26500 ENU10295 ANI61C3592: 3588	ANI61C3592: 3588			TBX	AFUc09097		5.2E-32	
26501 ENUI0296 ANI61C1093 2:1213582	ANI61C1093 2:1213582			TBX	AFUc15923		1.3E-49	
26502 ENU10297 ANI61C1093 6:22071787	ANI61C1093 6:22071787			TBX	AFUc05492		5.8E-53	
26503 ENUI0298 ANI61C1093 7:7821237	ANI61C1093 7:7821237			TBX	AFUc14290		2.1E-41	
26504 ENUI0299 ANI6ICI094 3:423671	ANI61C1094 3:423671			TBX	AFUc17390		6.5E-42	
26505 ENU10300 ANI61C2880: 800504	ANI61C2880: 800504			TBX	AFUc16447		1.2E-32	

Sec		Primer	Primer	Selection		aat Blast	Blast	%	
Seq id 36 ENU10301	Contig source ANI61C2882: 8081305	sod s	3 pos	Basis TBX	Database Hit ncbi gi AFUc13856	อ	Prob 2.1E-47	% id cvrg Description	
26507 ENUI0302 ANI61C2 481783	ANI61C2885: 481783			TBX	AFUc14906		7.3E-35		
26508 ENU10303 ANI61C1096 3:47204947	ANI61C1096 3:47204947			TBX	AFUc01385		2.5E-37		
26509 ENU10304 ANI61C1 4:6680	ANI61C1097 4:6680			TBX	AFUc09332		2E-40		
26510 ENUI0305 ANI61C1097 8:377102	ANI61C1097 8:377102			TBX	AFUc10468		8E-37		
26511 ENU10306 ANI61C9300: 24011704	ANI61C9300: 24011704			TBX	"AFUc05781, AFUc12769"		"2.7e-47, 2.6e-47"		
26512 ENU10307 ANI61C1 7:23202	ANI61C1098 7:23202655			TBX	AFUc21995		2.4E-46		
26513 ENU10308 ANI61C1 9:46918	ANI61C1098 9:46918			TBX	AFUc12150		4.4E-39		
26514 ENU10309 ANI61C9310: 74125	ANI61C9310: 74125			TBX	AFUc15016		4E-81		
26515 ENUI0310 ANI61C9318: 48384473	ANI61C9318: 48384473			TBX	AFUc07003		7.7E-89		
26516 ENU10311 ANI61C9326: 15641956	ANI61C9326: 15641956			TBX	AFUc15104		4.7E-65		
26517 ENU10312 ANI61C8605: 1497625	ANI61C8605: 1497625			TBX	AFUc06416		5.3E-44		
26518 ENU10313 ANI61C8 3240275	ANI61C8608: 32402755			TBX	AFUc04235		4.7E-50		
26519 ENU10314 ANI61C8608: 40913681	ANI61C8608: 40913681			TBX	AFUc01064		3.8E-53		

#### ocenio centro

Seq num Seq id Contig source 26520 ENU10315 ANI61C8615: 36413897	Contig source ANI61C8615: 36413897	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc15221	aat Blast Score Score	Blast Prob % 3.5E-54	% % id cvrg Description
26521 ENU10316 ANI61C9345: 3023	ANI61C9345: 3023			TBX	AFUc15332		3E-33	
26522 ENU10317 ANI61C8618: 28992618	ANI61C8618: 28992618			TBX	AFUc15281		1.8E-47	
26523 ENU10318 ANI61C8618: 35893119	ANI61C8618: 35893119			TBX	AFUc03740		8.5E-36	
26524 ENU10319 ANI61C9355: 5437	ANI61C9355: 5437			TBX	AFUc15687		9.2E-108	
26525 ENU10320 ANI61C9362: 19591529	ANI61C9362: 19591529			TBX	AFUc21030		1.2E-35	
26526 ENU10321 ANI61C9363: 1339866	ANI61C9363: 1339866			TBX	AFUc20167		2.7E-42	
26527 ENU10322 ANI61C8635: 14021717	ANI61C8635: 14021717			TBX	AFUc15942		3.1E-34	
26528 ENU10323 ANI61C9369: 24371592	ANI61C9369: 24371592			TBX	"AFUc01185, FGRc20865"		"6.1e-20, 2.0e-37"	
26529 ENU10324 ANI61C9377: 9551296	ANI61C9377: 9551296			TBX	AFUc08600		4.6E-38	
26530 ENU10325 ANI61C8649: 35683825	ANI61C8649: 35683825			TBX	"AFUc09782, FGRc24890"		"2.0e-21, 1.9e-43"	
26531 ENU10326 ANI61C8653: 20702574	ANI61C8653: 20702574			TBX	AFUc04641		8.6E-43	
26532 ENU10327 ANI61C8656: 20892426	ANI61C8656: 20892426			TBX	T18724		1.7e-22	
26533 ENU10328 ANI61C9386: 6502094	AN161C9386: 6502094			TBX	AFUc13410		8.1E-94	

% % id cvrg Description													
Blast Prob 2.7E-74	5.5E-57	9E-47	2.5E-89	2.1E-67	1.6E-37	7.1E-40	3.1E-48	5.2E-49	4.4E-34	5.7E-57	4.4E-68	4.9E-52	1.4E-81
Blast													
aat Score													
ncbi gi													
Database Hit AFUc10787	AFUc11560	AFUc05795	AFUc13321	AFUc13122	AFUc09860	AFUc03753	AFUc02330	AFUc08324	AFUc03634	AFUc05209	AFUc14948	AFUc02784	AFUc12855
	AFU	AFU	AFU	AFU	AFU	AFU	AFU	AFU	AFU	AFU	AFU	AFU	AFU
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 26534 ENU10329 ANI61C8659: 566294	26535 ENU10330 ANIGIC7939: 14401162	26536 ENU10331 ANIGIC8669: 40814653	26537 ENU10332 ANIGIC8672: 121160	26538 ENUI0333 ANI61C8685: 144353	26539 ENU10334 ANI61C7963: 25403006	26540 ENU10335 ANI61C7988: 556248	26541 ENUI0336 ANIGIC7994: 24063131	26542 ENUI0337 ANI61C5025: 1520773	26543 ENUI0338 ANI61C4311: 338670	26544 ENUI0339 ANIGIC5041: 132716	26545 ENUI0340 ANI61C4315: 26672467	26546 ENUI0341 ANI61C5049: 1100303	26547 ENUI0342 ANI61C5053: 7360

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26548 ENU10343 ANI61C3616: 1021686	Selection Basis TBX	Database Hit ncbi gi AFUc11581	aat Blast Score Score	Blast % Prob % id cv 2E-31	% id cvrg Description
26549 ENU10344 ANI61C5075: 9581185	TBX	AFUc14875		2.5E-141	
26550 ENU10345 ANI61C4346: 343761	TBX	AFUc04097		3.4E-34	
26551 ENU10346 ANI61C3623: 18892795	TBX	"AFUc11914, FGRc09621"		"1.9e-72, 9.4e-31"	
26552 ENU10347 ANI61C3623: 4008	TBX	AFUc15572		3.6E-44	
26553 ENU10348 ANI61C4360: 10291415	TBX	AFUc15474		1.7E-128	
26554 ENU10349 ANI61C3634: 8881166	TBX	AFUc14338		1.6E-116	
26555 ENU10350 ANI61C5094: 8361	TBX	AFUc08772		6.5E-38	
26556 ENU10351 ANI61C3637: 21451699	TBX	AFUc09606		5E-40	
26557 ENU10352 ANI61C2915: 29152528	TBX	AFUc11110		5.6E-35	
26558 ENU10353 ANI61C4374: 21492712	TBX	Z71256		1.4e-56	
26559 ENU10354 ANI61C3652: 2604	TBX	AFUc00801		3.7E-35	
26560 ENU10355 ANI61C2931: 8617	TBX	AFUc08105		1.6E-51	
26561 ENU10356 ANI61C3670: 9231135	TBX	AFUc11895		3.5E-39	

% id cvrg Description													
aat Blast Blast Score Score Prob % 6.4E-78	1.8E-49	8.5E-70	1E-67	1.6E-80	5.7E-34	2.7E-42	3.8E-34	2E-54	5.3E-55	3.1E-33	5.4E-55	3.6E-38	2E-135
n Database Hit ncbi gi AFUc15435	AFUc07056	AFUc10264	AFUc05625	AFUc13072	AFUc08724	AFUc03107	AFUc08363	AFUc14805	AFUc05950	AFUc14901	AFUc15792	AFUc06663	AFUc14363
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer ree 5 pos 3 pos 72:	49:	94:	: 98:	76:	82:	33:	:9435:	42:	8715: ,	16:	54:	28731: 388	33:
Seq num Seq id Contig source 26562 ENU10357 ANI61C3672: 455679	26563 ENU10358 ANI61C2949: 167850	26564 ENU10359 ANI61S2794: 559104	26565 ENU10360 ANI61C2968: 15212163	26566 ENU10361 ANI61C2976: 18612472	26567 ENU10362 ANI61C2982: 51510	26568 ENU10363 ANI61C9433: 998517	26569 ENU10364 ANI61C94; 44431	26570 ENU10365 ANI61C9442: 33062878	26571 ENU10366 ANI61C87 442867	26572 ENU10367 ANI61C8716: 13841013	26573 ENU10368 ANI61C9454: 22601922	26574 ENU10369 ANI61C873 16632388	26575 ENU10370 ANIGIC8733: 1307567

500		Drimer	Drimer	Calaction		22 Blact B	Blact	6
seq num Seq id 26576 ENU10371	Contig source ANI61C8739: 765463		3 pos	Basis TBX	Database Hit ncbi gi AFUc10121	re Score	50	% id cvrg Description
26577 ENU10372	ANI61C8739: 12681017			TBX	AFUc10121	4	4.2E-50	
26578 ENU10373 ANI61C8740: 63615553	ANI61C8740: 63615553			TBX	AFUc14582	.2	2.4E-87	
26579 ENU10374 ANI61C9478: 14471242	ANI61C9478: 14471242			TBX	FGRc11372	9	6.1E-49	
26580 ENU10375 ANI61C8751: 26252849	ANI61C8751: 26252849			TBX	AFUc08745	Ř	3.6E-45	
26581 ENU10376 ANI61C9484: 6711048	ANI61C9484: 6711048			TBX	AFUc11750	.2	2.5E-71	
26582 ENU10377 ANI61C9484: 10481296	ANI61C9484: 10481296			TBX	AFUc11750	.2	2.5E-71	
26583 ENU10378 ANI61C8768: 1699	ANI61C8768: 1699			TBX	AFUc06951	.9	6.8E-57	
26584 ENU10379 ANI61C8774: 16831354	ANI61C8774: 16831354			TBX	AFUc22116	I.	1.4E-40	
26585 ENU10380 ANI61C8775: 11691564	ANI61C8775: 11691564			TBX	FGRc11711	1.	1.1E-39	
26586 ENU10381 ANI61C5103: 771452	ANI61C5103: 771452			TBX	AFUc14207	6	9.4E-86	
26587 ENU10382 ANI61C4 2958316	ANI61C4415: 29583168			TBX	AFUc14631	5.	5.7E-117	
26588 ENU10383 ANI61C4 29027	ANI61C4415: 29027			TBX	AFUc08588	∞ <b>ʻ</b>	8.1E-50	
26589 ENUI0384 ANIGIC4421: 5821	ANI61C4421: 5821			TBX	AFUc13569	18	8E-83	

% % id cvrg Description 1,		•				_	4	_	_	10	~		16
Blast Prob "5.8e-31, 7.6e-11"	7.7E-32	9.8E-49	5.3E-83	7.2E-31	3E-125	1.6E-47	7.1E-47	7.2E-77	1.6E-37	8.9E-35	1.8E-68	3.2E-41	1.4E-45
Blast e Score													
aat Score													
Database Hit ncbi gi "AFUc01789, AFUc17092"	AFUc14561	AFUc08493	AFUc07782	AFUc10065	AFUc15520	AFUc01619	AFUc16279	AFUc12357	AFUc07536	AFUc06687	AFUc09976	AFUc16169	AFUc14515
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 26590 ENU10385 ANI61C5150: 7171240	26591 ENU10386 ANI61C4423: 12821818	26592 ENU10387 ANI61C5159: 698164	26593 ENU10388 ANI61C3704: 361854	26594 ENUI0389 ANI61C4437: 17272095	26595 ENU10390 ANI61C5173: 1175777	26596 ENU10391 ANI61C3725: 7291112	26597 ENU10392 ANI61C3734: 34558	26598 ENU10393 ANI61C3735: 20993050	26599 ENU10394 ANI61C4464: 4332	26600 ENU10395 ANI61C3736: 34243224	26601 ENU10396 ANI61C3737: 2813	26602 ENU10397 ANI61C3743: 62792	26603 ENU10398 ANI61C3747: 8601082

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26604 ENU10399 ANI61C3754: 49315320	Selection Basis TBX	Database Hit ncbi gi CALc04204	aat Blast Blast Score Score Prob 5.7E-83	% id cvrg Description
26605 ENU10400 ANI61C4494: 10561402	TBX	AFUc03670	2.3E-40	
26606 ENU10401 ANI61C3796: 23332704	TBX	AFUc14450	4.8E-34	
26607 ENU10402 ANI61C9500: 8036	TBX	AFUc15381	1.IE-73	
26608 ENU10403 ANI61C9533: 28822592	TBX	FGRc08616	6E-83	
26609 ENU10404 ANI61C8814: 61996564	TBX	AFUc16594	4E-32	
26610 ENU10405 ANI61C8818: 31443440	TBX	Y13135	2.9e-22	
26611 ENU10406 ANI61C8818: 22061928	TBX	AFUc13384	9.4E-45	
26612 ENU10407 ANI61C9551: 23182079	TBX	AFUc11576	3E-58	
26613 ENU10408 ANI61C9551: 30602512	TBX	AFUc11576	3E-58	
26614 ENU10409 ANI61C9554: 45854318	TBX	D50617	1.8e-18	
26615 ENU10410 ANI61C9556: 46094214	TBX	AFUc12874	2.1E-53	
26616 ENU10411 ANI61C9556: 52484933	TBX	AFUc12874	2.1E-53	
26617 ENU10412 ANI61C8837: 34322767	TBX	"AFUc00743, AFUc09194"	"1.8e-11, 9.3e-42"	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26618 ENU10413 ANI61C9577: 51535725	Selection Basis TBX	Database Hit ncbi gi AFUc20879	aat Blast Score Score	Blast Prob 2.9E-58	% id cvrg Description
26619 ENU10414 ANI61C9579: 21651657	TBX	"AFUc13295, FGRc06579"		"5.7e-31, 1.5e-12"	
26620 ENU10415 ANI61C9585: 845213	TBX	AFUc11738		6.2E-96	
26621 ENU10416 ANI61C8873: 1147668	TBX	AFUc04140		1.4E-46	
26622 ENU10417 ANI61C8876: 126374	TBX	Y13135		1.9e-146	
26623 ENU10418 ANI61C8878: 42573709	TBX	AFUc15197		1.1E-100	
26624 ENU10419 ANI61C5200: 13922379	TBX	"CALc06185, CALc06185"		"4.1e-37, 5.6e-13"	
26625 ENU10420 ANI61C5207: 48260	TBX	AFUc15608		1.5E-46	
26626 ENU10421 ANI61C5211: 2232	TBX	AFUc09688		2.8E-32	
26627 ENU10422 ANI61C5228: 44370	TBX	AFUc14750		1.2E-90	
26628 ENU10423 ANI61C5238: 983675	TBX	AFUc13449		1.1E-42	
26629 ENU10424 ANI61C5238: 17761549	TBX	AFUc13449		1.1E-42	
26630 ENU10425 ANI61C5240: 93863	TBX	AFUc14032		1E-65	
26631 ENU10426 ANI61C4514: 588343	TBX	AFUc08117		2.6E-31	

Seq num Seq id Contig source 26632 ENU10427 ANI61C5247: 49695199	Contig source ANI61C5247: 49695199	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi AFUc13730	aat Blast Score Score	Blast Prob 9 IE-97	% id cvrg Description
26633 ENU10428 ANI61C52 34778	ANI61C5248: 34778			TBX	AFUc14275		2.2E-43	
26634 ENU10429 ANI61C52 1324	ANI61C5250: 1324			TBX	AFUc07874		7.2E-35	
26635 ENU10430 ANI61C45 8131025	ANI61C4526: 8131025			TBX	AFUc15744		6.4E-115	
26636 ENU10431 ANI61C45 428664	ANI61C4534: 428664			TBX	AFUc02260		2E-47	
26637 ENU10432 ANI61C45 9351201	ANI61C4534: 9351201		•	TBX	AFUc02260		2E-47	
26638 ENU10433 ANI61C3809: 66327087	ANI61C3809: 66327087			TBX	AFUc16219		2.6E-60	
26639 ENU10434 ANI61C3822: 2610	ANI61C3822: 2610			TBX	AFUc11403		4.2E-59	
26640 ENU10435 ANI61C45 2343	ANI61C4556: 2343			TBX	AFUc08005		7.6E-41	
26641 ENU10436 ANI61C3830: 3292	ANI61C3830: 3292			TBX	FGRc22883		8.1E-33	
26642 ENU10437 ANI61C52 8871411	ANI61C5291: 8871411			TBX	AFUc02421		6.6E-51	
26643 ENU10438 ANI61C4576: 332673	ANI61C4576: 332673			TBX	AFUc14692		3.7E-38	
26644 ENU10439 ANI61C4579: 77666	ANI61C4579: 77666			TBX	AFUc08897		3.3E-63	
26645 ENU10440 ANI61C4581: 167460	ANI61C4581: 167460			TBX	AFUc10845		8.7E-34	

Seq num Seq id 26646 ENU10441	Contig source ANI61C4587: 4012	Primer 5 pos	Primer 3 pos	Selection Basis TBX	Database Hit ncbi gi FGRc06237	aat Blast Score Score	Blast Prob 2.7E-37	% id cvrg Description
26647 ENU10442 ANI61C3885: 7201126	ANI61C3885: 7201126			TBX	"AFUc05920, AFUc05920"		"1.6e-31, 7.0e-60"	
26648 ENU10443 ANI61C3890: 1104649	ANI61C3890: 1104649			TBX	AFUc09816		4.1E-48	
26649 ENU10444 ANI61C9618: 2465	ANI61C9618: 2465			TBX	AFUc03874		7.4E-63	
26650 ENU10445 ANI61C9634: 50664527	ANI61C9634: 50664527			TBX	AFUc02404		4.9E-39	
26651 ENU10446 ANI61C9636: 47264224	ANI61C9636: 47264224			TBX	"FGRc17533, Y13140"		"4.0e-28, 2.3e-26"	
26652 ENU10447 ANI61C9637: 1073178	ANI61C9637: 1073178			TBX	FGRc10589		4.6E-75	
26653 ENU10448 ANI61C8908: 23622835	ANI61C8908: 23622835			TBX	AFUc15919		3E-49	
26654 ENU10449 ANI61C8910: 3912	ANI61C8910: 3912			TBX	AFUc04556		3.7E-43	
26655 ENU10450 ANI61C8913: 34763057	ANI61C8913: 34763057			TBX	AFUc03973		1.5E-35	
26656 ENU10451 ANI61C9642: 1286852	ANI61C9642: 1286852			TBX	FGRc10508		2.7E-48	
26657 ENU10452 ANI61C8921: 22192962	ANI61C8921: 22192962			TBX	AFUc13687		2.4E-34	
26658 ENU10453 ANI61C8921: 52354886	ANI61C8921: 52354886			TBX	AFUc08999		3.6E-32	
26659 ENU10454 ANI61C9656: 23452824	ANI61C9656: 23452824			TBX	AFUc12498		6.1E-46	

Blast Blast % Score Prob % id cvrg Description 9.2E-38	1.2E-63	1.5E-56	"4.5e-12, 1.3e-33"	1.4E-60	6.7E-60	2.9E-47	2.9E-47	2.7E-50	1.2E-83	1.1E-33	6.9E-86	1.8E-35	5.8E-58
on Database Hit ncbi gi Score FGRc06110	AFUc11984	AFUc07937	"FGRc06761, FGRc13645"	AFUc14283	AFUc04448	AFUc03959	AFUc03959	FGRc11722	AFUc12092	FGRc02733	AFUc09469	AFUc19130	AFUc10229
Primer Primer Selection 5 pos 3 pos Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq num Seq id Contig source 5 26660 ENU10455 ANI61C8932: 6465	26661 ENU10456 ANI61C9663: 44383729	26662 ENU10457 ANI61C8941: 8371202	26663 ENU10458 ANI61C9673: 33512389	26664 ENU10459 ANI61C9683: 1130903	26665 ENU10460 ANI61C8956: 37043153	26666 ENU10461 ANI61C8958: 28231	26667 ENU10462 ANI61C8958: 512282	26668 ENU10463 ANI61C8962: 33003755	26669 ENU10464 ANI61C8966: 34854861	26670 ENU10465 ANI61C9697: 39703734	26671 ENU10466 ANI61C9698: 15651311	26672 ENU10467 ANI61C8971: 25270	26673 ENU10468 ANI61C8975: 60631

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26674 ENUI0469 ANI61C8980:	Selection Basis TBX		aat Blast % Score Score Prob % id cvrg Description 1.6E-114
26675 ENU10470 ANI61C8981: 61676614	TBX	AFUc15468	5.5E-156
26676 ENU10471 ANI61C8986: 54485828	TBX	AFUc17681	L.5E-36
26677 ENU10472 ANI61C8992: 43387	TBX	AFUc15788	6.5E-46
26678 ENU10473 ANI61C6020: 1131769	TBX	AFUc11116	1.4E-44
26679 ENU10474 ANI61C6020: 18041235	TBX	"AFUc11116, AFUc12982"	"1.4e-44, 5.6e-31"
26680 ENU10475 ANI61C6029: 470844	TBX	AFUc02496	7.2E-59
26681 ENU10476 ANI61S4401: 4495	TBX	Y13139	1.4e-16
26682 ENU10477 ANIGIC5311: 35093204	TBX	AFUc15777	7.9E-197
26683 ENU10478 ANI61C5312: 7361092	TBX	FGRc00937	2E-39
26684 ENU10479 ANI61C5313: 21843161	TBX	"AFUc08581, FGRc10546"	"1.3e-89, 1.9e-13"
26685 ENU10480 ANI61C5314: 8821340	TBX	AFUc14733	9.7E-42
26686 ENU10481 ANI61S4434: 5580	TBX	AFUc13932	4.8E-43
26687 ENU10482 ANI61C6060: 8524	TBX	AFUc15741	9.1E-144

## الامناوا والمتواوات

% % id cvrg Description													
aat Blast Blast Score Score Prob 1.3E-41	5.5E-32	2.5E-70	3.6E-53	8.6E-35	6.1E-57	1.5E-102	3.9E-38	9.3E-35	2.1E-40	1.8E-56	4.9e-16	8.5E-32	3.1E-152
on Database Hit ncbi gi AFUc18220	AFUc11752	AFUc02952	AFUc13396	AFUc15283	AFUc09536	AFUc14010	AFUc15201	AFUc08524	AFUc13777	AFUc12006	U00093	AFUc17957	AFUc15917
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer 5 pos 3 pos													
Seq num Seq id Contig source 26688 ENU10483 ANI61C5339: 17711418	26689 ENU10484 ANI61C5346: 12931616	26690 ENU10485 ANI61C3905: 1127333	26691 ENU10486 ANI61C3905: 15071292	26692 ENU10487 ANI61C6092: 510307	26693 ENU10488 ANI61C3908: 10131393	26694 ENU10489 ANI61C3916: 13311672	26695 ENU10490 ANI61C3922: 3212	26696 ENU10491 ANI61S3768: 482240	26697 ENU10492 ANI61C4662: 613335	26698 ENU10493 ANI61C4670: 74553	26699 ENU10494 ANI61C3958: 13671068	26700 ENU10495 ANI61C3964: 58796301	26701 ENUI0496 ANI61C3979: 11323123

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26702 ENU10497 ANI61C1002: 26913661	Selection Basis TBX	Database Hit ncbi gi AFUc11715	aat Blast Blast Score Score Prob 9E-91	% % id cvrg Description
26703 ENU10498 ANI61C1002: 20961689	TBX	AFUc03394	3.1E-34	4
26704 ENU10499 ANI61C3982: 9341254	TBX	AFUc15781	9.6E-174	74
26705 ENU10500 ANI61C1030: 24113198	TBX	AFUc10447	2.7E-51	
26706 ENU10501 ANI61C9702: 40684367	TBX	"AFUc10199, AFUc10199"	"1.4e-80, 6.8e-74"	
26707 ENU10502 ANI61C1072: 75413	TBX	AFUc15759	4.6E-43	3
26708 ENU10503 ANI61C9726: 6531	TBX	CALc05491	6.1E-33	3
26709 ENU10504 ANI61C9729: 22161656	TBX	AFUc14102	5.2E-39	6
26710 ENU10505 ANI61C9737: 34326	TBX	AFUc14470	6.8E-75	8
26711 ENU10506 ANI61C9737: 1274918	TBX	AFUc14470	6.8E-75	\$
26712 ENU10507 ANI61C9768: 12712131	TBX	U00094	3.0e-246	91
26713 ENU10508 ANI61C9771: 41194642	TBX	AFUc07319	3.7E-53	3
26714 ENU10509 ANI61C9776: 58485597	TBX	AFUc10732	1.6E-49	6
26715 ENU10510 ANI61C9779: 777364	TBX	Y13137	5.8e-80	

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26716 ENU10511 ANI61C9783:	Selection Basis TBX	n Database Hit ncbi gi AFUc13340	aat Blast Blast Score Score Prob 1.2E-31	% id cvrg Description
26717 ENU10512 ANI61C9791: 79397275	TBX	AFUc11371	4.4E-76	
26718 ENU10513 ANI61C9793: 14865	TBX	AFUc07854	1.4E-78	
26719 ENU10514 ANI61C6117: 11291617	TBX	AFUc09532	2.1E-48	
26720 ENUI0515 ANI61S4503: 57517	TBX	AFUc08015	3.8E-77	
26721 ENU10516 ANI61C5405: 35244	TBX	AFUc04307	6.2E-38	
26722 ENU10517 ANI61C6134: 666.878	TBX	AFUc12780	4.1E-49	
26723 ENU10518 ANI61C6136: 21702385	TBX	AFUc12645	8.3E-105	
26724 ENU10519 ANI61C6143: 3525	TBX	FGRc15010	5.3E-33	
26725 ENU10520 ANI61C5422: 209562	TBX	FGRc06384	1.1E-40	
26726 ENU10521 ANI61C4701: 32194	TBX	AFUc05559	3.7E-89	
26727 ENU10522 ANI61C6167: 85837	TBX	AFUc14614	1.4E-83	
26728 ENU10523 ANI61C6169: 533844	TBX	AFUc15069	1.2E-59	
26729 ENU10524 ANI61C4711: 8045	TBX	AFUc12529	1.2E-107	

aat Blast Blast % Score Score Prob % id cvrg Description 3.4E-32	1.4E-58	7.1E-38	1E-38	6.7E-68	3.3E-44	1.7E-128	1.6E-33	1.4E-103	1.2E-52	5.3E-36	3E-86	8E-40	5.1E-46
n Database Hit ncbi gi AFUc11891	AFUc07768	AFUc18477	AFUc13638	AFUc14210	AFUc14562	AFUc15821	AFUc15972	AFUc11693	AFUc00822	AFUc00901	AFUc15050	CALc06186	AFUc11351
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26730 ENU10525 ANI61C4714:	26731 ENU10526 ANI61C4721: 76363	26732 ENU10527 ANI61C6180: 9631289	26733 ENU10528 ANI61C4733: 77687	26734 ENU10529 ANIGICS462: 921253	26735 ENU10530 ANI61C5471: 6211014	26736 ENU10531 ANI61C4749: 16931490	26737 ENU10532 ANI61S4583: 51377	26738 ENU10533 ANI61C4764: 494195	26739 ENU10534 ANI61C4784: 1322855	26740 ENU10535 ANI61C4790: 720457	26741 ENU10536 ANI61C4796: 15582298	26742 ENU10537 ANIGIC1104: 1273611	26743 ENU10538 ANI61C1112: 27941976

aat Blast Blast % Score Score Prob % id cvrg Description 2.3E-56	1.1E-41	1E-105	3.1E-98	1.2E-120	1.2E-120	6.3E-91	6.3E-91	8.4E-44	1.9E-71	3.2E-40	9.8E-57	8.4E-80	2.9E-120
ion Database Hit ncbi gi CALc03518	AFUc15689	AFUc11947	AFUc15916	AFUc15972	AFUc15972	AFUc15803	AFUc15803	CALc06190	AFUc22467	AFUc13156	AFUc16697	AFUc15915	AFUc15848
Primer Primer Selection 5 pos 3 pos Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Seq Pour Contigue Pour Seq id Contigue Seq id	26745 ENU10540 ANI61C1120: 17901437	26746 ENU10541 ANI61C1127: 20141043	26747 ENU10542 ANI61C1135: 17662113	26748 ENU10543 ANI61C1137: 10315	26749 ENU10544 ANI61C1137: 4301264	26750 ENUI0545 ANI61C1138: 193701	26751 ENU10546 ANI61C1138: 16031989	26752 ENU10547 ANI61C1139: 53675110	26753 ENU10548 ANI61C1141: 20402351	26754 ENU10549 ANI61C9807: 23862132	26755 ENU10550 ANI61C1183: 32853707	26756 ENU10551 ANI61C1188: 2371	26757 ENU10552 ANI61C1188: 46904926

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26758 ENU10553 ANI61C1188:	Selection Basis TBX	Database Hit ncbi gi AFUc13465	aat Blast Blast Score Score Prob 2.6E-50	% id cvrg Description
26759 ENU10554 ANI61C9827: 49044662	TBX	AFUc01941	4.4E-33	
26760 ENU10555 ANI61C1190: 16691460	TBX	AFUc19119	3.3E-46	
26761 ENU10556 ANI61C9876: 48995639	TBX	AFUc01111	4.6E-51	
26762 ENU10557 ANI61C9878: 16701978	TBX	FGRc13922	3.2E-51	
26763 ENU10558 ANI61C9880: 44424932	TBX	AFUc19094	8.2E-36	
26764 ENU10559 ANI61C9880: 50385410	TBX	AFUc10800	2.7E-74	
26765 ENU10560 ANI61C9880: 1147719	TBX	AFUc20412	4.8E-39	
26766 ENU10561 ANI61C9882: 59256479	TBX	AFUc10536	1.3E-48	
26767 ENU10562 ANI61C9883: 17652013	TBX	AFUc03896	9.4E-34	
26768 ENU10563 ANI61C6208: 40054583	TBX	AFUc02427	6.4E-42	
26769 ENU10564 ANI61C6220: 228691	TBX	AFUc13617	7.9E-152	
26770 ENU10565 ANI61S4601: 36916	TBX	AFUc17622	9.7E-46	
26771 ENU10566 ANI61C5501: 19052144	TBX	CALc02466	3.2E-69	

aat Blast Blast % Score Score Prob % id cvrg Description 2.1E-57	3.5E-35	2.6E-96	7.3E-37	9.4E-66	4.9E-31	1.1e-52	"5.2e-76, 1.6e-18"	3.3E-51	3.2E-62	1.3E-52	2.7E-118	3.4E-45	1.9E-36
n Database Hit ncbi gi AFUc13011	AFUc15725	AFUc14374	AFUc05656	AFUc12895	AFUc12576	Y13134	"AFUc14618, FGRc25347"	AFUc17116	AFUc10520	AFUc12278	AFUc09182	AFUc02495	AFUc05031
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer Primer ce 5 pos 3 pos 4:	2:	ö	4:	:8	·0	3:	%:	3:	·6	ö	5:	·6	4:
Seq num Seq id Contig source 26772 ENU10567 ANI61C5504: 7191018	26773 ENU10568 ANI61C5512: 1004735	26774 ENU10569 ANI61C5520: 7953	26775 ENU10570 ANI61C5524: 4799	26776 ENU10571 ANI61C6258: 25951909	26777 ENU10572 ANI61C6260: 36472	26778 ENU10573 ANI61C5533: 28153542	26779 ENU10574 ANI61C4808: 1828.2380	26780 ENU10575 ANI61C5543: 286621	26781 ENU10576 ANI61C6279: 9921635	26782 ENU10577 ANI61C4820: 1166402	26783 ENU10578 ANI61C4825: 3263	26784 ENU10579 ANI61C4829: 541759	26785 ENU10580 ANI61C6294:

% id cvrg Description													
Blast Prob 2.2E-59	2.3E-41	7.1E-59	1.1E-58	3.3E-48	6.8E-127	2.2E-64	6.1E-58	"7.2e-48, 3.7e-60, 5.5e-50"	1.7e-114	1.7e-114	1.7e-114	3E-223	"2.5e- 220, 3.0e- 223"
Blast Score	``	•	·	•	•	•			•			``	
aat Score													
ncbi gi													
Database Hit ncbi gi AFUc13847	AFUc14576	AFUc11703	AFUc14922	AFUc12427	AFUc15187	AFUc11440	AFUc18745	"AFUc00755, AFUc11547,	Y13137	Y13137	Y13137	AFUc15972	"AFUc15972, AFUc15972"
Selection Basis TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX	TBX
Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 26786 ENU10581 ANI61C6299: 6031086	26787 ENU10582 ANI61S3944: 5361	26788 ENU10583 ANI61C4841: 161523	26789 ENU10584 ANI61C4844: 1224514	26790 ENU10585 ANI61C5574: 42874858	26791 ENU10586 ANI61C4851: 13591936	26792 ENU10587 ANI61C4852: 465217	26793 ENU10588 ANI61C4858: 42253968	26794 ENU10589 ANI61C1213: 6662015	26795 ENU10590 ANI61C1002 1:20422257	26796 ENU10591 ANI61C1002 1:28073483	26797 ENU10592 ANI61C1002 1:50435705	26798 ENU10593 ANI61C1233: 104469	26799 ENU10594 ANI61C1233: 5932227

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% % id cvrg Description aat Blast Blast Score Score Prob Database Hit ncbi gi Selection Basis I GSP Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26816 ENU10611 ANI61C4238: 1653..2569

26817 ENU10612 ANI61C9758: 5232..2829

GSP

26818 ENU10613 ANI61C9777: 4913..3682

GSP

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Primer 3 pos			
Primer Primer 5 pos 3 pos			
Seq num Seq id Contig source 26819 ENU10614 ANI61C9272: 28054329	26820 ENU10615 ANI61C1120 5:35055508	26821 ENU10616 ANI61C1136 8:39563354	26822 ENU10617 ANI61C3922: 2211201
Seq num 26819	26821	2682	2682;

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26823 ENU10618 ANI61C4244:

Selection Basis I GSP

Database Hit ncbi gi

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26824 ENUI0619 ANI61C9662: 1762..3272

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26825 ENU10620 ANI61C1189: 733..2186

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Selection Basis GSP	GSP	GSP	GSP
Primer 3 pos			
Primer Primer 5 pos 3 pos			
Seq num Seq id Contig source 26826 ENU10621 ANI61C852:1 0551534	26827 ENU10622 ANI61C1018 8:25241832	26828 ENU10623 ANIGIC1106 4:44675468	26829 ENU10624 ANI61C1037 9:25583166
Conti ANIG 055	8:252	4:446	+ ANI6 9:255
id J10621	J10622	J10623	J10624
Seq 26 ENI	27 EN	S EN	29 ENI
Seq num 2682	2682	2682	2682

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% id cvrg Description aat Blast Blast Score Score Prob Database Hit ncbi gi Selection Basis I GSP Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26830 ENU10625 ANI61C8159: 1418..708

26831 ENU10626 ANI61C4204: 4458..1758

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26832 ENU10627 ANI61C9269: 447..1520

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% % id cvrg Description aat Blast Blast Score Score Prob Database Hit ncbi gi Selection Basis I GSP Seq Primer Primer Primer num Seq id Contig source 5 pos 3 pos 26833 ENU10628 ANI61C1174:

26834 ENU10629 ANI61C1099 8:6512..4967

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26835 ENU10630 ANI61C3343: 3012..1656

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Primer 5 pos		
Seq num Seq id Contig source 5 26836 ENU10631 ANI61C1023 6:1381026	ANI61C9178: 41543195	ANI61C8787: 2798117
n Seq id 36 ENU10631	26837 ENU10632 ANI61C9178: 41543195	26838 ENU10633 ANI61C8787: 2798117
Seq nun 268	268	268

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26839 ENU10634 ANI61C1052 2:9..1581

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% % id cvrg Description aat Blast Blast Score Score Prob Database Hit ncbi gi Selection Basis I GSP Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26840 ENU10635 ANI61C391:1 157..2307

26841 ENU10636 ANI61C8594: 354..1610

GSP

26842 ENUI0637 ANI61C5881: 796..2073

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% % id cvrg Description aat Blast Blast Score Score Prob Database Hit ncbi gi Selection Basis I GSP Primer Primer 5 pos 3 pos Seq num Seq id Contig source 5 pos 26843 ENU10638 ANI61C1067 6:1673..506

GSP

26844 ENU10639 ANIGIC1026 6:639..1493 26845 ENU10640 ANI61C9273: GSP 2356..3502

26846 ENU10641 ANI61C9135: 1310..282

GSP

Cultum Callantica

Selection Basis I GSP Seq Primer Primer Primer num Seq id Contig source 5 pos 3 pos 26847 ENU10642 ANI61C4057:

Database Hit ncbi gi

aat Blast Blast Score Score Prob

% id cvrg Description

26848 ENU10643 ANIGIC5181: 205..730

GSP

26849 ENU10644 ANI61C5163: 1648..925

GSP

26850 ENU10645 ANI61C9611: 1060..208

GSP

## ngungan nopo

%	% id cvrg Description
Blast	Prob
Blast	Score
aat	Score
	ncbi gi
	Database Hit
Selection	Basis GSP
Primer	3 pos
Primer	5 pos
	num Seq id Contig source 26851 ENU10646 ANI61C6211: 58483572
	Seq id ENU1064
Seq	num 26851

26852 ENU10647 ANI61C3390: GSP 1827...500

26853 ENU10648 ANI61C405:2 GSP 513..1849

26854 ENU10649 ANI61C8967: GSP 1333..2100

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Selection Basis Database Hit ncbi gi SGSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
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Seq Primer num Seq id Contig source 5 pos 26855 ENU 10650 ANI 61 C 6915: 231 1067	26856 ENU10651 ANI61C9116: 45115203	26857 ENU10652 ANI61C2197: 153952	26858 ENU10653 ANI61C1026 9:34352	26859 ENU10654 ANI61C309:1 6242155	26860 ENU10655 ANI61C1027 9:33253609	26861 ENU10656 ANI61C1480: 94427	26862 ENU10657 ANI61C1029 5:27642435	26863 ENU10658 ANI61C7211: 17551192	26864 ENU10659 ANI61C7220: 12871690

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n Database Hit ncbi gi											
Selection Basis GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer Primer 5 pos 3 pos											
Seq num Seq id Contig source 5 26865 ENU10660 ANI61C7233: 157435	26866 ENU10661 ANI61C6507: 4121250	26867 ENU10662 ANI61C7239: 19871316	26868 ENU10663 ANI61C7239: 34004598	26869 ENU10664 ANI61C9301: 8751414	26870 ENU10665 ANI61C7262: 35719	26871 ENU10666 ANI61C6551: 551973	26872 ENU10667 ANI61C5824: 1441000	26873 ENU10668 ANI61C5838: 1710790	26874 ENU10669 ANI61S229:2 1272	26875 ENU10670 ANI61C6580: 9541271	26876 ENU10671 ANI61S247:4 1818

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Database Hit ncbi gi										
Selection Basis GSP GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer 3 pos	8 9 4 - 4 1 7									
Seq Primer num Seq id Contig source 5 pos 26877 ENU10672 ANI61C6599: 22191887 26878 ENU10673 ANI61S277:1	41353 26879 ENUI0674 ANI61C1106 7:35833283 5 5 6	26880 ENU10675 ANI61C2213: 58810	26881 ENU10676 ANI61C2215: 78497241	26882 ENU10677 ANI61C2223: 191631	26883 ENU10678 ANI61C2224: 498845	26884 ENU10679 ANI61C2229: 29857	26885 ENU10680 ANIGIC1102 0:27540	26886 ENU10681 ANI61C1505: 482971	26887 ENU10682 ANI61C1030 0:9731299	26888 ENU10683 ANI61C1103 6:21321698

Seq		Primer	Primer	Selection		aat ]	Blast	Blast	%	
Seq id 39 ENU10684	Contig source ANI61C1030 9:539240	5 pos	3 pos	Basis GSP	Database Hit ncbi gi	Score	Score	Prob	% id cvrg	Description
26890 ENU10685 ANI61 8:8033	ANI61C1103 8:80337008			GSP						
26891 ENU10686 ANI61 6:427.	ANI61C1031 6:427146			GSP						
26892 ENU10687 ANI61C2268: 67622	ANI61C2268: 67622			GSP						
26893 ENUI0688 ANI61C1033 2:196702	ANI61C1033 2:196702			GSP						
26894 ENU10689 ANI61C1033 2:18572930	ANI61C1033 2:18572930			GSP						
26895 ENU10690 ANI61 7:692.	ANI61C1106 7:692997			GSP						
26896 ENU10691 ANI61C1106 9:14881817	ANI61C1106 9:14881817			GSP						
26897 ENU10692 ANI61C1106 9:42554617	ANI61C1106 9:42554617			GSP						
26898 ENU10693 ANI61S1377: 44411	ANI61S1377: 44411			GSP						
26899 ENU10694 ANI61C1553: 11031303	ANI61C1553: 11031303			GSP						
26900 ENUI0695 ANIGICI108 3:728460	ANI61C1108 3:728460			GSP						
26901 ENU10696 ANI61C2291: 173520	ANI61C2291: 173520			GSP						
26902 ENU10697 ANI61C2297: 622891	ANI61C2297: 622891			GSP						

Seq num Seq id 26903 ENU10698	Seq id Contig source 3 ENU10698 ANI61C1036	Primer 5 pos	Primer 3 pos	Selection Basis GSP	n Database Hit ncbi gi	ncbi gi	aat Score	Blast Score	Blast Prob	% % id cvrg	% % id cvrg Description
1:0952102 26904 ENU10699 ANIGIC1036 3:30812758	1:0952/102 ANI61C1036 3:30812758			GSP							
26905 ENUI0700 ANI61C1109 8:804166	ANT61C1109 8:804166			GSP							
26906 ENUI0701 ANI61C425:6 27833	ANI61C425:6 27833			GSP							
26907 ENUI0702 ANI61C8007: 408139	ANI61C8007: 408139			GSP							
26908 ENU10703 ANI61C7305: 13652019	ANI61C7305: 13652019			GSP							
26909 ENU10704 ANI61C7309: 528756	ANI61C7309: 528756			GSP							
26910 ENU10705 ANI61C474:3	ANI61C474:3 7324			GSP							
26911 ENU10706 ANI61C7312: 392165	ANI61C7312: 392165			GSP							
26912 ENU10707 ANI61C485:5 84121	ANI61C485:5 84121			GSP							
26913 ENU10708 ANI61C6606: 379762	ANI61C6606: 379762			GSP							
26914 ENUI0709 ANI61C8075: 17442038	ANI61C8075: 17442038			GSP							
26915 ENU10710 ANI61C8086: 10381379	ANI61C8086: 10381379			GSP							
26916 ENUI0711 ANI61C7373: 53197	ANI61C7373: 53197			GSP							

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Seq num Seq id Contig source 26928 ENU10723 ANI61C2339: 45935853	Primer 5 pos	Primer 3 pos	Selection Basis GSP	Database Hit ncbi gi	aat Score	Blast	Blast Prob	% id cvrg	% cvrg	Description
26929 ENUI0724 ANI61S1445: 217447			GSP							
26930 ENUI0725 ANI61C7400: 25031237			GSP							
26931 ENU10726 ANI61C3077: 67214			GSP							
26932 ENU10727 ANI61C1041 1:563261			GSP							
26933 ENUI0728 ANI61S1452: 35918			GSP							
26934 ENU10729 ANI61C2352: 176792			GSP							
26935 ENU10730 ANI61S1463: 28674			GSP							
26936 ENU10731 ANI61C2361: 93460			GSP							
26937 ENU10732 ANI61C2361: 30523372			GSP							
26938 ENU10733 ANI61C1116 5:16452411			GSP							

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26939 ENU10734 ANI61C2372: 8551133	r Selection Basis GSP	tion Database Hit ncbi gi	aat Score	Blast Score	Blast Prob	% % id cvrg Description	ion
26940 ENU10735 ANI61C2372: 16522011	GSP						
26941 ENU10736 ANI61C1045 4:45704971	GSP						
26942 ENU10737 ANI61C1661: 882424	GSP						
26943 ENUI0738 ANI61C1047 4:160561	GSP						
26944 ENUI0739 ANI61C1047 5:35312	GSP						
26945 ENU10740 ANI61C1686: 634265	GSP						
26946 ENUI0741 ANI61C511:3 2511	GSP						
26947 ENU10742 ANI61C511:9 552004	GSP						
26948 ENU10743 ANI61C515:5 071530	GSP						
26949 ENU10744 ANI61C517:6 3610	GSP						
26950 ENU10745 ANI61C1697: 907698	GSP						
26951 ENU10746 ANI61C531:3 131072	GSP						
26952 ENUI0747 ANI61C534:3 22579	GSP						

GSP

GSP

26963 ENU10758 ANI61C6717: 3333..2875

26964 ENUI0759 ANI61C6721: 881..525

GSP

26975 ENUI0770 ANI61C2435:

4559..4236

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 26976 ENU10771 ANIG1C2438: 28803290	L	Selection Basis Database Hit ncbi gi GSP	aat Score	Blast	Blast Prob	% id cvrg	g Description
26977 ENU10772 ANI61C1716: 392141	GSP	۵.					
26978 ENU10773 ANI61C1051 8:69129	GSP	۵					
26979 ENU10774 ANI61C2452: 1114866	GSP	۵					
26980 ENU10775 ANI61C1052 9:71500	GSP	Q.					
26981 ENU10776 ANI61C2462: 29382609	GSP	۵					
26982 ENU10777 ANI61C1053 2:32247	GSP	۵					
26983 ENU10778 ANI61C1740: 17481434	GSP	۵					
26984 ENU10779 ANI61C2478: 93382	GSP	۵					
26985 ENU10780 ANI61C2488: 122484	GSP	ā.					
26986 ENU10781 ANI61C1128 1:107430	GSP						
26987 ENU10782 ANI61S1594: 2153	GSP	Q.					
26988 ENU10783 ANI61C1056 2:35878	GSP	۵					
26989 ENUI0784 ANI61C1057 5:448687	GSP	<b>Q</b> .					

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on Database Hit ncbi gi											
Selection Basis GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer Primer 5 pos 3 pos											
Seq Prinum Seq id Contig source 5 p 27016 ENU10811 ANI61C6825: 11101553	27017 ENU10812 ANI61C6826: 8921134	27018 ENU10813 ANI61C8285: 6801088	27019 ENUI0814 ANI61C1118 8:1202234	27020 ENUI0815 ANI61C6833: 47594	27021 ENU10816 ANI61C6845: 12251545	27022 ENU10817 ANI61C6869: 44449	27023 ENU10818 ANI61C6876: 1362467	27024 ENU10819 ANI61S544:2 9629	27025 ENU10820 ANI61C3201: 14632118	27026 ENU10821 ANI61C3206: 90620	27027 ENUI0822 ANI61C3220: 676904

# C) (3) (4) (4) (5) (5) (6) (7) (6) (7) (9) (9)

Seq I Contig source 27042 ENU10837 ANI61C2551: 593144	Primer Primer 5 pos 3 pos	Selection Basis Database Hit ncbi gi GSP	aat Blast Blast Score Score Prob	% % id cvrg Description
27043 ENU10838 ANI61C1825: 96480		GSP		
27044 ENU10839 ANI61C1827: 63511		GSP		
27045 ENU10840 ANI61C2557: 35811		GSP		
27046 ENU10841 ANI61S1665: 22514		GSP		
27047 ENU10842 ANI61C2564: 1021556		GSP		
27048 ENU10843 ANI61C2564: 30003693		GSP		
27049 ENU10844 ANI61C2565: 18431553		GSP		
27050 ENU10845 ANI61C1136 0:423744		GSP		
27051 ENU10846 ANI61C1136 1:314753		GSP		
27052 ENU10847 ANIGIC1136 5:61594		GSP		
27053 ENU10848 ANI61C1137 0:1053437		GSP		

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3 pos											
Primer 5 pos											
Seq num Seq id Contig source 27054 ENU10849 ANI61C9801: 9361955	27055 ENU10850 ANI61C1851: 23713	27056 ENU10851 ANIGIC1859: 689332	27057 ENU10852 ANI61C1065 0:2568	27058 ENU10853 ANI61C1066 6:40318	27059 ENU10854 ANI61C701:1 24521	27060 ENU10855 ANI61C705:5 73153	27061 ENU10856 ANI61C9000: 29613380	27062 ENU10857 ANI61C1887: 209448	27063 ENU10858 ANI61C9010: 11961606	27064 ENU10859 ANI61C1893: 30260	27065 ENU10860 ANI61C738:7 25203

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Selection Basis Database Hit ncbi gi GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Seq Primer Primer num Seq id Contig source 5 pos 3 pos 27066 ENU10861 ANI61C749:5 6721	27067 ENU10862 ANT61C8311: 1091738	27068 ENU10863 ANI61C757:1 84432	27069 ENU10864 ANI61C8057: 25-47 1810-39741828	1:	27071 ENU10866 ANI61C7603: 27602347	27072 ENU10867 ANIGIC9066: 29782667	27073 ENU10868 ANI61C9077: 44074640	27074 ENU10869 ANIGIC8352: 1633964	27075 ENU10870 ANIGIC7626: 13662139	27076 ENU10871 ANIGIC7627: 17901413	27077 ENU10872 ANI61C6902: 58303	27078 ENU10873 ANI61C6902: 8491115	27079 ENU10874 ANIGIC7631: 30399	27080 ENU10875 ANI61C9094: 1157593

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Seq num Seq id Contig source 27081 ENU10876 ANI61C6912: 14831817	27082 ENUI0877 ANI61C7644: 445945	27083 ENU10878 ANI61C8385: 774119	27084 ENU10879 ANI61C6940: 16852623	27085 ENU10880 ANI61S606:3 3278	27086 ENU10881 ANI61C7683: 56815	27087 ENU10882 ANI61C7685: 651899	27088 ENU10883 ANI61C6973: 58857	27089 ENU10884 ANI61C4000: 24362718	27090 ENUI0885 ANI61C38:27 804266	27091 ENU10886 ANI61C6988: 65479	27092 ENU10887 ANI61C4014: 12811520	27093 ENU10888 ANI61C47:51 659	27094 ENU10889 ANI61C4030: 795365

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Selection Basis GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer 3 pos						755-777								
Primer 5 pos						25-46								
Seq num Seq id Contig source 27095 ENU10890 ANI61C4033: 64360	27096 ENU10891 ANI61S3149: 137451	27097 ENU10892 ANI61C4041: 33770	27098 ENU10893 ANI61C3319: 449210	27099 ENUI0894 ANIGIC87:13 60758	27100 ENU10895 ANI61C90:28383	27101 ENU10896 ANI61C9734: 25-46	27102 ENU10897 ANIGIC4069: 483163	ANI61C1140 4:30571670	27104 ENU10899 ANIGIC1140 5:362983	27105 ENU10900 ANI61C1140 8:481109	27106 ENU10901 ANI61C4075: 1168899	27107 ENU10902 ANI61S1726: 161580	27108 ENU10903 ANIGIC2623: 7691152	27109 ENU10904 ANI61C3354: 1852823
seq id 95 ENU10890	96 ENU10891	97 ENU10892	98 ENU10893	99 ENU10894	00 ENU10895	01 ENU10896	02 ENU10897	27103 ENU10898 ANI61C1140 4:30571670	04 ENU10899	05 ENU10900	06 ENU10901	07 ENU10902	08 ENU10903	09 ENU10904
Seq num 2709	2709	2709	2709	2709	271(	271(	271(	271(	271(	271(	271(	271(	271(	271(

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tion . Database Hit ncbi gi														
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Primer 3 pos			,					1184-						
Primer 5 pos								25-43						
Seq num Seq id Contig source 27110 ENU10905 ANI61C4083: 600292	27111 ENU10906 ANI61C2631: 56996	27112 ENU10907 ANI61C2634: 57563	27113 ENU10908 ANI61C4098: 31192841	27114 ENU10909 ANI61C1143 7:27363185	27115 ENU10910 AM61C1911: 743462	27116 ENU10911 ANI61C1917: 658913	27117 ENU10912 ANI61C3375: 274515	27118 ENU10913 ANI61C726:1 25-43 5192739	27119 ENU10914 ANI61C3384: 522319	27120 ENU10915 ANI61C1145 3:1122904	27121 ENU10916 ANI61C1072 6:39550	27122 ENU10917 ANI61S1762: 138449	27123 ENU10918 ANI61C1072 8:504109	27124 ENU10919 ANI61C1145 8:498226

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Primer Primer 5 pos 3 pos													5-45 1020-	1
Seq num Seq id Contig source 5 27125 ENU10920 ANI61C1936: 12491759	27126 ENU10921 ANI61C3394: 5071723	27127 ENU10922 ANI61C3396: 134527	27128 ENU10923 ANI61C1939: 555292	27129 ENU10924 ANI61C1146 3:26803042	27130 ENU10925 ANI61S1771: 153362	27131 ENU10926 ANI61C2671: 31923	27132 ENU10927 ANI61C2672: 34605	27133 ENU10928 ANI61C1074 6:16451439	27134 ENU10929 ANI61C1950: 26509	27135 ENU10930 ANI61C1955: 8411119	27136 ENU10931 ANI61C1077 3:30442808	27137 ENU10932 ANI61C1987: 42125	27138 ENU10933 ANI61C9739: 25-45	27139 ENU10934 ANIGIC815:5 05807

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Primer 3 pos													
Primer 5 pos													
Seq num Seq id Contig source 5 27140 ENU10935 ANI61C9119: 670385	27141 ENU10936 ANI61C1993: 578104	27142 ENU10937 ANI61C1079 7:39323549	27143 ENU10938 ANI61C9132: 954398	27144 ENU10939 ANI61C840:4 9456	27145 ENU10940 ANI61C849:1 1871681	27146 ENU10941 ANI61C876:1 5902086	27147 ENU10942 ANI61C7712: 422293	27148 ENU10943 ANI61C9179: 68016508	27149 ENU10944 ANI61C881:8 191067	27150 ENU10945 ANI61C7726: 18112377	27151 ENU10946 ANI61C9186: 5461025	27152 ENU10947 ANI61C7728: 17352	27153 ENU10948 ANI61C8461: 1237130

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 27154 ENU10949 ANI61C7733: 5451042	r Selection Basis GSP	n Database Hit ncbi gi	aat Score	Blast Score	Blast Prob	% % id cvrg Description
27155 ENU10950 ANI61C8464: 23692686	GSP					
27156 ENU10951 ANI61C9194: 50945	GSP					
27157 ENU10952 ANI61C7738: 7731078	GSP					
27158 ENU10953 ANI61C8477: 600325	GSP					
27159 ENU10954 ANI61C7750: 935549	GSP					
27160 ENU10955 ANI61C8483: 27391493	GSP					
27161 ENU10956 ANI61C7758: 5821060	GSP					
27162 ENU10957 ANI61C8488: 24202040	GSP					
27163 ENU10958 ANI61S10:38 8158	GSP					
27164 ENU10959 ANI61C7772: 17792054	GSP					
27165 ENU10960 ANI61S704:2 9069	GSP					
27166 ENU10961 ANI61C7784: 33440	GSP					
27167 ENU10962 ANI61S3210: 133504	GSP					

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Selection Basis GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer 3 pos							1462-	È						
Primer 5 pos	·						25-48							
Contig source ANI61S54:41 684	27169 ENU10964 ANI61S57:40 527	27170 ENU10965 ANI61C4111: 381989	27171 ENU10966 ANI61C4118: 1219627	27172 ENU10967 ANI61S62:39 2105	27173 ENU10968 ANIGIC4136: 18202838	27174 ENU10969 ANI61S80:90. .302	27175 ENU10970 ANI61C8145: 25-48 4252575	ANI61S786:8 5726	27177 ENU10972 ANIGLC2704: 18301507	27178 ENU10973 ANIGIC4171: 169876	27179 ENU10974 ANI61C3448: 29325	27180 ENU10975 ANIGIC3467: 38222	27181 ENU10976 ANIGIC3469: 29429	27182 ENU10977 ANI61C2740:
Seq num Seq id Contig source 27168 ENU10963 ANI61S54:41 684	ENU10964	ENU10965	ENU10966	ENU10967	ENU10968	ENU10969	ENU10970	27176 ENU10971 ANI61S786:8 5726	ENU10972	s ENU10973	ENU10974	ENU10975	ENU10976	: ENU10977
Seq num 27168	27169	27170	27171	27172	27173	27174	27175	27176	77172	27178	27179	27180	27181	27182

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seq num Seq id Contig source 27183 ENU10978 ANI61C2762: 566303		3 pos	Selection Basis GSP	Database Hit ncbi gi	Score	Score 1	blast Prob	% % id cvrg Description
27184 ENU10979 ANI61C6697: 25-46	: 25-46	428-456 GSP	GSP					
27185 ENU10980 ANIGIS1889: 276489			GSP					
27186 ENU10981 ANI61C1085 3:9123556			GSP					
27187 ENU10982 ANI61C1085 7:388684			GSP					
27188 ENU10983 ANI61C2796: 6511025			GSP					
27189 ENU10984 ANI61C910:2 3432119	61		GSP					
27190 ENU10985 ANI61C1088 3:1002601			GSP					
27191 ENU10986 ANI61C9218: 232642			GSP					
27192 ENU10987 ANI61C927:2 5382790	6)		GSP					
27193 ENU10988 ANI61C9232: 3961202			GSP					
27194 ENU10989 ANI61C944:1 4831128	_		GSP					
27195 ENU10990 ANI61C8518: 971204			GSP					
27196 ENU10991 ANI61C950:3 5647	8		GSP					
27197 ENU10992 ANI61C8529: 41914479			GSP					

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Selection Basis GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer 3 pos												1200-	/771	
Primer 5 pos												25-48		
Contig source ANI61C963:1 0681394	27199 ENU10994 ANI61C9261: 7231335	27200 ENU10995 ANI61C8533: 199436	27201 ENU10996 ANI61C8534: 38314522	27202 ENU10997 ANI61C8539: 16032387	27203 ENU10998 ANI61C8543: 32982891	27204 ENU10999 ANIGIC7818: 15251	27205 ENU11000 ANI61C9283: 75970	27206 ENU11001 ANI61C9284: 569336	27207 ENU11002 ANI61C9284: 22391572	27208 ENU11003 ANI61C7852: 17259	27209 ENUI1004 ANIGIC7868: 1327541	27210 ENU11005 ANI61C7532: 25-48	27211 ENUI1006 ANI61C7889: 134827	27212 ENU11007 ANI61C4201: 651966
Seq num Seq id 27198 ENU10993	27199 ENU109	27200 ENU109	27201 ENU109	27202 ENU109	27203 ENU109	27204 ENU109	27205 ENU110	27206 ENU110	27207 ENU110	27208 ENU110	27209 ENU110	27210 ENULIO	27211 ENU110	27212 ENU110

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Primer 3 pos						2512-								
Primer 5 pos						5-50								
Seq num Seq id Contig source 5 27213 ENU11008 ANI61C4231: 10452050	27214 ENU11009 ANI61C4240: 18021443	27215 ENU11010 ANI61S870:7 5413	27216 ENU11011 ANI61S887:5 3371	27217 ENU11012 ANI61S1900: 24236	27218 ENU11013 ANI61S3362: 59322	27219 ENU11014 ANI61C4253: 25-50 3902994	27220 ENU11015 ANI61C2823: 703311	27221 ENU11016 ANI61S1936: 3307	27222 ENU11017 ANIGIC3564: 27412421	27223 ENU11018 ANI61C4294: 94511	27224 ENU11019 ANI61C1090 3:24082130	27225 ENU11020 ANI61C1090 9:12071480	27226 ENU11021 ANI61C3574: 621271	27227 ENU11022 ANI61C2851: 33880

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Seq num Seq id Contig source 27228 ENU11023 ANI61S1970: 107523	27229 ENU11024 ANI61S1976: 45338	27230 ENU11025 ANI61C1094 6:29713210	27231 ENU11026 ANI61C1095 9:6921021	27232 ENU11027 ANI61C1097 4:86518980	27233 ENU11028 ANI61C9307: 20601566	27234 ENUI1029 ANI61C9309: 71346	27235 ENU11030 ANI61C1098 8:22182525	27236 ENU11031 ANI61C9318: 10561424	27237 ENU11032 ANI61C9320: 21601305	27238 ENU11033 ANI61C8612: 28923431	27239 ENU11034 ANI61C9350: 97312	27240 ENU11035 ANI61C8622: 26193263	27241 ENU11036 ANI61C7901: 15591341

Seq num Seq id Contig source 27257 ENU11052 ANI61C3604: 172483	Primer 5 pos	Primer 3 pos	Selection Basis GSP	Database Hit ncbi gi	aat E Score S	Blast   Score	Blast Prob	% % id cvrg Description	ption
27258 ENU11053 ANI61C5067: 52811			GSP						
27259 ENU11054 ANI61C4339: 641103			GSP						
27260 ENU11055 ANI61S3440: 24733			GSP						
27261 ENU11056 ANI61C4340: 1106646			GSP						
27262 ENU11057 ANI61C8097: 25-52		572-597	GSP						
27263 ENU11058 ANIGLC3625: 410209			GSP						
27264 ENU11059 ANI61C4355: 231006			GSP						
27265 ENU11060 ANI61S986:2 4416			GSP						
27266 ENU11061 ANI61S987:2 30502			GSP						
27267 ENU11062 ANI61C2904: 49527			GSP						
27268 ENU11063 ANI61C5091: 39426			GSP						
27269 ENU11064 ANI61C5092: 565249			GSP						
27270 ENU11065 ANI61C5099: 16941380			GSP						
27271 ENU11066 ANI61S3475: 3422			GSP						

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Seq Primer Primer Primer num Seq id Contig source 5 pos 3 pos 27302 ENU11097 ANIG1C4426:	L	Selection Basis Database Hit ncbi gi GSP	aat Score	Blast	Blast Prob	% % id cvrg De	Description
27303 ENU11098 ANI61S2803: 83411	g	GSP					
27304 ENUI1099 ANI61C4434: 7891070	9	GSP					
27305 ENU11100 ANI61C3707: 581356	9	GSP					
27306 ENU11101 ANI61C4437: 18581610	9	GSP					
27307 ENU11102 ANI61S4274: 82586	9	GSP					
27308 ENUIII03 ANI61C4445: 61133	9	GSP					
27309 ENU11104 ANI61C4451: 567883	9	GSP					
27310 ENU11105 ANI61C3725: 13411595	9	GSP					
27311 ENU11106 ANI61S2831: 24825	9	GSP					
27312 ENU11107 ANI61S3566: 727473	9	GSP					
27313 ENU11108 ANI61S4296: 106351	9	GSP					
27314 ENU11109 ANI61C3734: 8511099	9	GSP					
27315 ENU11110 ANI61S2840: 557300	9	GSP					

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 27316 ENUIIIII ANI61C3754:	Selection Basis Database Hit ncbi gi GSP	aat Blast Blast Score Score Prob	t % % id cvrg Description
27317 ENU11112 ANI61C3761: 33389	GSP		
27318 ENUIIII3 ANI61C3784: 637260	GSP		
27319 ENU11114 ANI61C3784: 9721225	GSP		
27320 ENU11115 ANI61C3791: 28648	GSP		
27321 ENU11116 ANI61C9503: 1086832	GSP		
27322 ENUIII17 ANI61C8804: 20376	GSP		
27323 ENU11118 ANI61C9553: 57546136	GSP		
27324 ENU11119 ANI61C8826: 10282376	GSP		
27325 ENU11120 ANI61C9579: 588247	GSP		
27326 ENU11121 ANI61C8850: 1149554	GSP		
27327 ENU11122 ANI61C9580: 31192889	GSP		
27328 ENU11123 ANI61C8890: 30062620	GSP		
27329 ENU11124 ANI61C8891: 15471314	GSP		

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 27330 ENU11125 ANI61C5220:	Selection Basis I GSP	Database Hit ncbi gi	aat Score	Blast Score	Blast Prob	% % id cvrg Description	ion
27331 ENU11126 ANI61C5238: 81503	GSP						
27332 ENUIII27 ANI6IC5252: 6051027	GSP						
27333 ENU11128 ANI61C4533: 1007711	GSP						
27334 ENUIII29 ANI6IC4533: 22621912	GSP						
27335 ENU11130 ANI61C3806: 151459	GSP						
27336 ENUIII31 ANI61C3809: 63676092	GSP						
27337 ENU11132 ANI61C3812: 34816	GSP						
27338 ENU11133 ANI61C3815: 562307	GSP						
27339 ENU11134 ANI61C3815: 66326285	GSP						
27340 ENU11135 ANI61C5276: 5031318	GSP						
27341 ENUIII36 ANI6IS4389: 224466	GSP						
27342 ENU11137 ANI61C4583: 4691	GSP						
27343 ENU11138 ANI61C4597: 36254	GSP						

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Seq num Seq id Contig source 51 27344 ENU11139 ANI61C4598: 26116	27345 ENU11140 ANI61C3886: 1166825	27346 ENU11141 ANI61C3899: 60866	27347 ENUIII42 ANI6IC9645: 52055854	27348 ENU11143 ANI61C9648: 1307840	27349 ENUIII44 ANI6IC8929: 1859827	27350 ENU11145 ANI61C8933: 116088	27351 ENU11146 ANI61C8942: 950555	27352 ENUIII47 ANI6IC8948: 816145	27353 ENU11148 ANI61C9689: 786439	27354 ENU11149 ANI61C9699: 20471317	27355 ENUIII50 ANI61C7193: 25-47	27356 ENUIII51 ANI61C6005: 9601552	27357 ENUIII52 ANIGIC6014: 45231	27358 ENU11153 ANIGIC5308: 11041550

# توقيد والاسكاب والاستابات

Ç	Primer Primer	Colection			ţċ	Blace	Blact	B	
Seq id Contig source 59 ENU11154 ANI61C6037: 45452		Basis GSP	Database Hit ncbi gi	ncbi gi	Score		Prob	% id cvrg	Description
27360 ENUIII55 ANI61C6049: 26432927		GSP							
27361 ENU11156 ANI61C6054: 617180		GSP							
27362 ENU11157 ANI61C5326: 269673		GSP							
27363 ENU11158 ANI61C6063: 548247		GSP							
27364 ENUI1159 ANI61C4630: 121563		GSP							
27365 ENUILI60 ANIGLC5365: 9851310		GSP							
27366 ENUILI61 ANI61S4484: 249611		GSP							
27367 ENUILI62 ANIGLC3921: 9531335		GSP							
27368 ENUIII63 ANI6IC3921: 27792390		GSP							
27369 ENU11164 ANI61C4653: 20871719		GSP							
27370 ENUILI65 ANIGLC4654: 16141315		GSP							
27371 ENU11166 ANI61C4658: 914174		GSP							
27372 ENUILI67 ANI61S3763: 74559		GSP							

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Seq Page 1 Contigue Poly Page 1 Contigue Poly Poly Poly Poly Poly Poly Poly Poly	Primer Primes 5 pos 3 pos	<b>.</b>	Selection Basis GSP	Database Hit ncbi gi	Score	Blast	Blast Prob	% id cvrg Description	
27374 ENUII169 ANI61C3933: 549114			GSP						
27375 ENU11170 ANI61C3937: 797354			GSP						
27376 ENUIII71 ANI61C3940: 21232			GSP						
27377 ENU11172 ANI61C3954: 13261063			GSP						
27378 ENU11173 ANI61C4685: 757491			GSP						
27379 ENU11174 ANI61C3958: 50189			GSP						
27380 ENU11175 ANI61C4696: 28056			GSP						
27381 ENU11176 ANI61C1004: 20192340			GSP						
27382 ENUIII77 ANI61C1014: 33063527			GSP						
27383 ENUII178 ANI61C3998: 32373			GSP						
27384 ENU11179 ANI61C1032: 460155			GSP						
27385 ENUIII80 ANI61C1050: 13191113			GSP						
27386 ENUIII81 ANI61C1081: 596850			GSP						

Seq         Primer         Primer         Selection           27387 ENUIII 82 ANIGICI0881:         5 pos 3 pos 6 GSP         3 pos 6 GSP         3 pos 6 GSP         4 pos 6 Score Prob 6 GSP           27388 ENUIII 82 ANIGICI0881:         4 bos 6.5         25.448         810-840         GSP         8 core Prob 6 Score Prob 6 GSP           27389 ENUII 84 ANIGICARD 85 ENUII 85 ANIGICARD 85 ENUII 85 ANIGICARD 85 ENUII 86 EN	% % id cvrg Description														
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5 pos         3 pos         Selection           5 pos         3 pos         Basis           25-48         810-840         GSP           25-48         810-840         GSP           4         GSP         GSP           5         GSP         GSP           6         GSP         GSP           7         GSP         GSP           8         GSP         GSP           8         GSP         GSP           9         GSP         GSP           9         GSP         GSP <trr< td=""><td>aat Score</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></trr<>	aat Score														
5 pos         3 pos         Selection           5 pos         3 pos         Basis           25-48         810-840         GSP           25-48         810-840         GSP           4         GSP         GSP           5         GSP         GSP           6         GSP         GSP           7         GSP         GSP           8         GSP         GSP           8         GSP         GSP           9         GSP         GSP           9         GSP         GSP <trr< td=""><td>ncbi gi</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></trr<>	ncbi gi														
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	Primer 3 pos		810-840												
	Primer 5 pos		25-48												
	Seq id Contig source 7 ENU11182 ANI61C1081: 17171370	188 ENUIII83 ANI61C1088: 48665	889 ENUIII84 ANI61C9367:	5701483 190 ENUIII85 ANIGIC9731: 1230467	391 ENU11186 ANI61C9798: 26182337	92 ENU11187 ANI61C6101: 8893	93 ENU11188 ANI61C6110: 85723	194 ENUIII89 ANI61C6122: 16182008	95 ENU11190 ANI61C6131: 1130355	196 ENU11191 ANI61C5407: 71948	197 ENU11192 ANI61C5427: 773264	98 ENU11193 ANI61C4706: 860402	199 ENU11194 ANI61C4711: 15951891	100 ENU11195 ANI61C4715: 142424	101 ENU11196 ANI61S3828: 200523

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Seq Primer Primer num Seq id Contig source 5 pos 3 pos 27402 ENU11197 ANI61S3837: 675343	L	Selection Basis GSP	Database Hit ncbi gi	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
27403 ENU11198 ANI61C6195: 47660	Ū	GSP							
27404 ENU11199 ANI61C4750: 755522	Ū	GSP							
27405 ENU11200 ANI61C4753: 1269856	Ū	GSP							
27406 ENU11201 ANI61C5487: 642219	Ū	GSP							
27407 ENU11202 ANI61C4762: 97372	Ū	GSP							
27408 ENU11203 ANI61C4787: 12301449	Ū	GSP							
27409 ENUI1204 ANI61C1100: 115802	Ū	GSP							
27410 ENU11205 ANI61C1111: 45545	Ū	GSP							
27411 ENU11206 ANI61C1111: 36794110	Ū	GSP							
27412 ENU11207 ANI61C1120: 78238526		GSP							
27413 ENU11208 ANI61C1169: 843553		GSP							
27414 ENU11209 ANI61C9822: 1217123		GSP							
27415 ENU11210 ANI61C9829: 40243818	J	GSP							

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Seq id Contig source 5 pos 16 ENU11211 ANI61C1192: 9741474		Database Hit ncbi gi	re Score	% id cvrg Description
27417 ENU11212 ANI61C9847: 61996726	GSP			
27418 ENU11213 ANI61C9867: 106634	GSP			
27419 ENU11214 ANI61C9891: 452243	GSP			
27420 ENU11215 ANI61C9899: 47334	GSP			
27421 ENU11216 ANI61C6223: 92463	GSP			
27422 ENU11217 ANI61S4621: 277516	GSP			
27423 ENU11218 ANI61C5522: 613402	GSP			
27424 ENU11219 ANI61C6258: 40174280	GSP			
27425 ENU11220 ANI61C4802: 2914	GSP			
27426 ENU11221 ANI61C5533: 11311565	GSP			
27427 ENU11222 ANI61C5535: 16692031	GSP			
27428 ENU11223 ANI61C6268: 16091048	GSP			
27429 ENU11224 ANI61C4818: 105579	GSP			

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Primer 3 pos	1030-												
Primer 5 pos	25-42												
Seq id Contig source 0 ENU11225 ANI61C6280: 695384	27431 ENU11226 ANIGIC1085 5:1314247 27432 ENU11227 ANIGIC6289: 635118	27433 ENU11228 ANI61C5562: 115501	27434 ENU11229 ANI61C4861: 232549	27435 ENU11230 ANI61C4883: 540944	27436 ENU11231 ANI61C4886: 692387	27437 ENU11232 ANI61C4888: 73528	27438 ENU11233 ANI61C1000 5:1846	27439 ENUI1234 ANIGIC1212: 24201437	27440 ENU11235 ANI61C1212: 72937081	27441 ENU11236 ANI61C1215: 1067828	27442 ENU11237 ANI61C1001 9:66374	27443 ENU11238 ANIGIC1001 9:14311786	27444 ENU11239 ANI61S1058: 46356
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Primer 3 pos		1027-	069-909	434-453	296-321	723-747	736-762	1159-	605-630	1770-	598-624	693-723	487-516	1124-	473-492	822-843	829-855
Primer 5 pos		25-47	25-49	25-43	25-50	25-48	25-50	25-48	25-53	25-48	25-54	25-54	25-49	25-56	25-51	25-42	25-44
4)	1 ANI61C1004 2:147493	27447 ENU11242 ANI61C3535: 25-47 2371526	27448 ENU11243 ANI61C5361: 25-49		27450 ENU11245 ANIGIC8290: 25-50 534196	27451 ENU11246 ANI61C8406: 25-48	27452 ENUI1247 ANI61C3560: 25-50		27454 ENU11249 ANI61C9335: 25-53	24319: 90		ANI61C9630: 60265230	27458 ENUI1253 ANIGIC3:451 25-49	1 27459 ENU11254 ANI61C3101: 25-56 381916	27460 ENU11255 ANI61C7406: 25-51 933.374	27461 ENU11256 ANIGIC2199: 25-42 8081	C1140 1670
Seq num Seq id Contig source 27445 ENU11240 ANI61C1002 4:388146	27446 ENU11241 ANI61C1004 2:147493	27447 ENU1124.	27448 ENU1124.	27449 ENU11244 ANI61C1043 6:45164046	27450 ENU1124.	27451 ENU1124	27452 ENU1124	27453 ENU11248	27454 ENU1124	27455 ENU1125	27456 ENU11251 ANI61C1135 4:73897	27457 ENU11252	27458 ENUI125	27459 ENU1125	27460 ENU1125.	27461 ENU1125	27462 ENUI1257 ANI61 4:2738

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Primer 3 pos 664-693	2514-	1048-	347-372	588-612	1031-	571-597	1674-	1714-	1740 773-807	957-984	549-573	481-504	1174-	550-579	506-534	312-339	697-726	1173-
Seq Primer num Seq id Contig source 5 pos 27463 ENU11258 ANI61C6375: 25-48	70780 27464 ENU11259 ANI61C3570: 25-47 4375 1718	27465 ENU11260 ANIGIC8506: 25-53 17022790	27466 ENU11261 ANI61C5:911 25-44	27467 ENU11262 ANIGIC2228: 25-47	27468 ENUI1263 ANI61C1229: 25-52 1066312053	27469 ENU11264 ANI61C2474: 25-48	27470 ENU11265 ANIG1C3401: 25-44 38191936	27471 ENU11266 ANIG1C7804: 25-49	24/1009 27472 ENU11267 ANI61C1413: 25-52	43853561 27473 ENU11268 ANI61C1078 25-48	0.2202308 27474 ENU11269 ANIGIC3185: 25-47 2066 1480	27475 ENUI1270 ANIGIC9745: 25-50	27476 ENU11271 ANI61C1075 25-48 6:8642078	27477 ENU11272 ANI61C8415: 25-53	2473.2142 27478 ENU11273 ANI61C147:1 25-59	27479 ENU11274 ANIGIC8168: 25-45	27480 ENUI1275 ANI61C297:5 25-47 607 4879	27481 ENUI1276 ANIGIC6326: 25-46 28291254

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Primer 3 pos 639-663 1057- 1086 1246- 1269	1062 1117- 1146 733-750 1232- 1254 979-1005	797-819 1279- 1311 493-516 810-834	758-780 395-423 2459- 2490 836-858	473-495 1066- 1098 1075- 1092
5 pos 25-51 25-52 25-43 25-42	25-45 25-49 25-43 25-48	25-53 25-43 25-51 25-50	25-47 25-49 25-48 25-51	25-43 25-56 25-45
Contig source ANIGIC1044 6:71946514 ANIGIC8003: 18181891 ANIGIC8107: 7132196	1321272 27486 ENU11281 ANIGIC1232: 27241345 27487 ENU11282 ANIGIC1097 27488 ENU11283 ANIGIC5397: 10952412 27489 ENU11284 ANIGIC3282:	1591181 27490 ENU11285 ANIGIC9348: 32992421 27491 ENU11286 ANIGIC4800: 18323077 27492 ENU11287 ANIGIC4256: 56633 27493 ENU11288 ANIGIC1134 6:1472487	711479:3 7479:3 6489: 76	90965 ANIGIC5742: 957452 ANIGIC1141 9:1511266 ANIGIC35:19
Seq num Seq id 27482 ENU11277 27483 ENU11278 27484 ENU11279 27485 ENU11280	27486 ENUI1281 27487 ENUI1282 27488 ENUI1283 27489 ENUI1284	ENU11285 ENU11286 ENU11287 ENU11288	27494 ENUI1289 27495 ENUI1290 27496 ENUI1291 27497 ENUI1292	27498 ENU11293 27499 ENU11294 27500 ENU11295
Seq num 27482 27483 27484 27485	27486 27487 27488 27489	27490 27491 27492 27493	27494 27495 27496 27497	27498 27499 27500

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Primer 3 pos 412-438 1601- 1632 862-891	1167 324-345 872-897 589-618	438-459 685-711 625-654 405-435	1428- 1458 674-699 487-510 609-630	571-594 1010- 1035 906-939 341-366
5 pos 25-48 25-50 25-51 25-53	25-51 25-47 25-55	25-48 25-50 25-52 25-48	25-46 25-48 25-45 25-45	25-54 25-50 25-48 25-48
ource 9640: 5944: 4 1072: 58		27508 ENU11303 ANIGIC1040 4:34943038 27509 ENU11304 ANIGIC3663: 53781 27510 ENU11305 ANIGIC8074: 17602561 27511 ENU11306 ANIGIC8623: 48015229	27512 ENU11307 ANIGLC9552: 29081237 27513 ENU11308 ANIGLC6472: 135851 27514 ENU11309 ANIGLC1041 7:7351262 27515 ENU11310 ANIGLC1006: 21442787	27516 ENU11311 ANI61C8909: 25-54 22202828 27517 ENU11312 ANI61C895:3 25-50 0781361 27518 ENU11313 ANI61C7397: 25-48 7963 27519 ENU11314 ANI61C5665: 25-48
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Primer 3 pos 517-543	907-930	597-630	1093-	1116 543-567	755-780	2275-	445-468	808-828	660-684	267-291	1486-	1935-	627-645	906-930	858-885	276-300	488-513	1289- 1314
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Primer 3 pos 1454-	272-303	585-615	941-969	398-420	732-759	1250-	773-795	1264-	565-597	951-975	1005-	540-564	520-552	1009-	1032 664-681	666-296	391-414	1288- 1314
Seq Primer num Seq id Contig source 5 pos 27539 ENU11334 ANI61C7855: 25-48 5514065	27540 ENU11335 ANI61C8464: 25-47	27541 ENU11336 ANI61C7650: 25-53 1237711	27542 ENU11337 ANI61C5313: 25-57	27543 ENUI1338 ANIGIC3043: 25-46	27544 ENUII339 ANI61CI139: 25-47	27545 ENU11340 ANI61C598:2 25-43 020685	27546 ENUII341 ANI61C3699: 25-46	27547 ENU11342 ANI61C9796: 25-48 2338 905	27548 ENUII343 ANI61C1118 25-45	27549 ENUII344 ANI61C8725: 25-43	27550 ENUI1345 ANI61C9321: 25-43	27551 ENU11346 ANI61C58:13 25-48	27552 ENUI1347 ANI61C5896: 25-43	27553 ENU11348 ANI61C1880: 25-47	27554 ENU11349 ANI61C768:4 25-44	27555 ENU11350 ANI61C4397: 25-44	27556 ENUI1351 ANI61C893:3 25-45	27557 ENU11352 ANI61C9103: 25-58 27111350

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Primer 3 pos 497-522	424-450	655-678	541-573	755-774	584-609	295-321	229-255	1005-	1029 531-555	911-939	1058-	963-990	1760-	381-405	542-567	511-537	907-933	396-423
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Primer 5 pos 25-47	25-49	25-44	25-47	25-47	25-52	25-49	25-46	25-42	25-49	25-50	25-48	25-53	25-43	25-45	25-43	25-44	25-46	25-54
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5 pos 25-46 25-54 25-57 25-57 25-50 25-50 25-40	25-49 25-49 25-47 25-47 25-47 25-57 25-57 25-51 25-51
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Primer 3 pos 504-528	1140- 1158 1439-	1461 520-549	194-216 1514- 1545	628-660	1045-	381-414	190-210	903-927	574-597	1163-	655-684	684-708	407-429	1044-	1218-
Primer 5 pos 25-50	25-47	25-48	25-48	25-48	25-48	25-47	25-44	25-44	25-49	25-43	25-55	25-53	25-46	25-44	25-60
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Primer 5 pos 25-47	25-53	25-56	25-60	25-42	25-49	25-45	25-45	25-46	25-49	25-48	25-48	25-45	25-55	25-47	25-52	25-49	25-46	25-48
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Primer 3 pos 403-426	729-756	515-540	879-903	748-774	225-255	788-807	538-561	343-369	834-855	755-777	307-336	475-498	416-438	321-342	411-438	249-273	410-438	2570- 2589
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Primer 3 pos 354-375	413-444	1090-	227-249	261-288	2030- 2055	238-270	292-315	499-519	250-285	778-807	907-933	1465- 1494	405-432	485-507	1236- 1263	1031-	325-360	729-759
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Primer 3 pos 500-525	396-423	1146	1296 1409-	633-660	821-846	228-252 1103-	1128 334-354	492-522	704-735	406-432	579-603	1757-	280-303	583-606	469-495	771-795
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Primer 3 pos 876-894	831-852	481-304	2398-	1873-	787-816	771-789	339-369	729-759	508-528	445-468	514-543	966-626	371-390	1005-	278-300	269-291	412-432
Primer 5 pos 25-50	25-46	25-49	25-49	25-49	25-48	25-48	25-45	25-49	25-47	25-44	25-45	25-56	25-42	25-50	25-45	25-53	25-43
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Primer 5 pos 25-48	25-44	25-51	25-51	25-45	25-47	25-50	25-52	25-46	25-48	25-54	25-47	25-48	25-44	25-52	25-55	25-52	25-52	25-52
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Primer 3 pos 382-405	454-477	583-606	285-309	664-687	954-975	409-432	177-201	289-699	388-411	334-357	280-300	631-657	893-915	189-222	531-558
Primer 5 pos 25-47	25-47	25-53	25-44	25-43	25-47	25-49	25-48	25-47	25-44	25-46	25-49	25-49	25-49	25-49	25-52
Seq num Seq id Contig source 27805 ENU11600 ANI61C9357: 51324710	27806 ENU11601 ANI61C1017 6:196787 27807 ENU11602 ANI61C1093	1:788.214 27808 ENU11603 ANI61C7422: 25712159 27809 ENU11604 ANI61C6595:	54365909 27810 ENU11605 ANI61C9031: 25-44 9831370	27811 ENU11606 ANI61C8413: 25-43 1182426 27812 ENU11607 ANI61C882:1 25-55	1101792 27813 ENU11608 ANI61C7049: 1571452	27814 ENUI1609 ANIGIC8615: 25-49 25862137	27815 ENU11610 ANI61C4383: 25-48 12871505	27816 ENU11611 ANI61C3047: 25-47 20843034	27817 ENU11612 ANI61C8629: 25-44 131609	27818 ENU11613 ANI61C6429: 82887822	27819 ENU11614 ANI61S2494: 34831	27820 ENU11615 ANI61C1133 9:8311678	27821 ENU11616 ANI61C2236: 20453023	27822 ENU11617 ANI61C4676: 136375	27823 ENU11618 ANI61C7181: 25-52 61385402

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Selection Basis Database Hit ncbi gi Sv GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer S 3 pos B 333-366 G	306-336 G	440-468 G	620-645 G	338-366 G	541-564 G	301-330 G	1106- G		121	521-543 G	266-291 G	574-597 G	806-828 G	240-273 G	734-765 G	483-507 G	897-921 G	783-813 G
Seq Primer num Seq id Contig source 5 pos 27824 ENU11619 ANI61C551:1 25-49	29884: 25-56	7826 ENU11621 ANI61C7815: 25-53	27827 ENU11622 ANI61C6422: 25-48 25273257	27828 ENUI1623 ANI61C810:6 25-51	27829 ENUI1624 ANI61C7484: 25-49 876, 1532	27830 ENUII625 ANI61C6594: 25-51	27831 ENUI1626 ANI61C672:4 25-48 3673026	27832 ENUI1627 ANIGIC1042 25-46 9-478 3694	27833 ENUI1628 ANIGIC1029 25-45	27834 ENU11629 ANI61C8774: 25-53	27835 ENU11630 ANIGIC8623: 25-49	27836 ENU11631 ANI61C8329: 25-55	27837 ENU11632 ANI61C7077: 25-45	27838 ENUI1633 ANIGIC8247: 25-49	27839 ENUI1634 ANI61C7270: 25-50	27840 ENUI1635 ANI61C9153: 25-49	27841 ENU11636 ANGICG778: 25-51	1769513 27842 ENU11637 ANI61C6947: 25-45 19731073

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Selection Basis GSP GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
Primer 3 pos 1106-1137 2174-	2193 1038- 1065 1262-	1287 802-834	1405- 1428 781-804	776-801	915-942 1179- 1206	1074- 1098	1064- 1083	842-870 755-783	1076-	950-972	887-912	1207- 1233	1483- 1506
Primer 5 pos 25-49 25-43	25-52	25-48	25-47	25-48	25-57	25-48	25-46	25-50 25-49	25-53	25-53	25-44	25-56	25-48
Seq num Seq id Contig source 27843 ENU11638 ANI61C6579: 943141 27844 ENU11639 ANI61C8732:	23:1 356:	2662348 ANI61C4797: 37922825	27848 ENU11643 ANI61C5384: 25-47 1988286 27849 FNI11644 ANI61C2961: 25-47	27850 ENU11645 ANI61C22:16 25-48 50714	27851 ENU11646 ANI61C7033: 25-57 1285233 27852 ENU11647 ANI61C7999: 25-52 38081181	27853 ENU11648 ANI61C8740: 25-48 131868	27854 ENU11649 ANI61C8379: 24501302	.; ö	1873.3008 27857 ENU11652 ANIGIC1060 4:2227993				27861 ENU11656 ANI61C1107 3:23944134

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Selection Basis Dat GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP	GSP
tion	2266- GSP 2298		10	843-864 GSP		1458 756-786 GSP		1038 844-861 GSP	973-996 GSP	788-810 GSP	1005- GSP		88	1035- GSP 1059	110	1230- GSP	263	1414- GSP 1434
Selection Basis GSP						98,												

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Database Hit	
Selection Basis GSP	GSP GSP GSP
Primer 3 pos 1176-1200 1504-1533 1068 1065-1089 925-948 775-795 969-996 1025-1025-1138-1328-1356 886-909 916-939 11338-1133	1113 1182- 1209 1300- 1323 825-849
Primer 5 pos 25-46 25-46 25-46 25-48 25-48 25-42 25-48 25-42 25-48 25-51 25-51 25-51 25-52 25-54 25-54 25-54 25-54 25-54 25-54 25-54	25-50 25-45 25-46
Seq num Seq id Contig source 27881 ENU11676 ANI61C8587: 3568833 27882 ENU11677 ANI61C7113: 1162566 27883 ENU11678 ANI61C217.7 123714 27884 ENU11680 ANI61C217.7 27885 ENU11680 ANI61C2779: 27886 ENU11681 ANI61C2779: 27891 ENU11682 ANI61C2748: 16252642 27889 ENU11683 ANI61C9702: 27890 ENU11685 ANI61C9303: 27891 ENU11685 ANI61C9303: 27892 ENU11686 ANI61C1430: 55846726 27893 ENU11688 ANI61C1430: 55846726 27894 ENU11689 ANI61C1109 9:56406853 27895 ENU11690 ANI61C1943: 27895 ENU11691 ANI61C9343: 1526	C1120 4364 C5332: 226 C1025

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aat Score																														
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n Database Hit ncbi gi						U51272	U75428	X84015	U34740	U12427	AB014886	AF019254	Z68905	M59705	Z68904	U34740	U03904	U83658	X82827	U75347	AF032987	U40146	AF016850	AJ003163	AF112473	U25693	X82289	U34740	D21268	U56100
Selection Basis GSP	GSP	GSP	GSP	GSP	GSP	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS
Primer 3 pos 2135-	808-837	857-888	1119-	1149 919-942	834-858	751-779	756-779	761-779	754-779	756-779	750-779	755-779	754-779	752-779	756-779	751-779	750-779	756-779	747-779	756-779	748-779	749-779	756-779	750-779	754-779	756-779	754-779	755-779	752-779	751-779
Primer 5 pos 25-51	25-55	25-51	25-49	25-42	25-48	42-64	26-43	22-45	48-71	40-63	37-60	37-60	34-57	31-54	31-54	29-54	29-52	28-51	26-49	26-46	25-48	25-48	24-47	24-47	24-47	24-51	23-47	23-46	23-51	22-44
Contig source ANI61C9323: 6303909	ANI61C4871:	ANI61C9878:	:9/	10312327 ANI61C6064:	21644140 ANI61C6256: 52074223																									
Seq num Seq id 27900 ENU11695	27901 ENU11696	27902 ENU11697	27903 ENU11698	27904 ENU11699	27905 ENU11700	27906 ENU11701	ENU11702	27908 ENU11703	27909 ENUI1704	27910 ENUI1705	ENU11706	ENU11707	ENU11708	ENU11709	ENU11710	ENU11711	ENU11712	ENU11713	27919 ENUI1714	27920 ENU11715	ENU11716	ENU11717	ENU11718	ENU11719	ENU11720	ENU11721	ENU11722	ENU11723	ENU11724	ENU11725
Seq num 3 27900 I	27901	27902	27903	27904	27905	27906	27907	27908	27909	27910	27911	27912	27913	27914	27915	27916 ]	27917	27918	27919	27920	27921	27922	27923	27924	27925	27926	27927	27928	27929	27930 ]

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	Database Hit U75347	D83246	U62895	AB000125	U52362	M58289	M83232	Y15996	D10019	X15441	U63728	Z80341		AF041976		U28804		L41670		AJ001836		X15479		N89675		Z49834		U59148		M16371		AF055287		U21220		AF02/213	
Selection	Basis CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS		CDS		CDS		CDS		CDS		CDS		CDS		CDS		CDS		CDS		CDS		CDS	i i	CDS	
Primer	3 pos 752-779	750-779	744-779	758-779	750-779	747-779	757-779	750-779	712-729	712-738	845-867	1004-	1026	1021-	1038	1099-	9111	1257-	1275	1257-	1275	1321-	1344	1383-	1404	1389-	1413	1404-	1425	1606-	1626	1643-	1662	1661	2016	2041-	2064
	5 pos 22-50	22-48	22-45	22-51	22-48	22-48	22-57	22-45	25-42	25-53	25-48	25-48		25-45		25-49		25-44		25-44		25-48		25-50		25-43		25-45		25-45		25-48		25-44		25-46	
	Contig source																																				
	Seq 1d 31 ENU11726	32 ENU11727	33 ENU11728	27934 ENUI1729	27935 ENU11730	27936 ENU11731	37 ENU11732	38 ENU11733	39 ENU11734	40 ENU11735	27941 ENU11736	42 ENU11737		27943 ENU11738		27944 ENU11739		27945 ENU11740		27946 ENU11741		27947 ENU11742		27948 ENUI1743		27949 ENU11744		27950 ENU11745		27951 ENU11746		27952 ENU11747		27953 ENU11748		27954 ENUII749	
Seq	num 27931	27932	27933	2793	2793	2793	27937	27938	27939	27940	2794	27942		2794		2794		2794		2794		2794		2794		2794		2795		2795		2795		2795	į	279.	

Seq		Primer	Primer	Selection			aat	Blast	Blast	%	
num Seq id 27955 ENU11750	Contig source	5 pos 25-46	3 pos 2074-	Basis CDS	Database Hit U70731	ncbi gi	Score	Score	Prob	% id cvrg	Description
			2097	Ç							
27956 ENUII751		25-46	2574- 2601	CDS	M58291						
27957 ENU11752		25-46	300-321	CDS	M96993						
27958 ENUI1753		25-45	365-390	CDS	U12632						
27959 ENU11754		25-45	377-402	CDS	X55547						
27960 ENU11755		25-46	404-429	CDS	J05545						
27961 ENU11756		25-50	418-441	CDS	X13525						
27962 ENU11757		25-50	418-441	CDS	X04696						
27963 ENU11758		25-48	443-462	CDS	U75874						
27964 ENU11759		25-49	497-525	CDS	D32070						
27965 ENU11760		25-45	573-600	CDS	X08866						
27966 ENU11761		25-53	630-657	CDS	Z49892						
27967 ENU11762		25-51	646-672	CDS	AJ001837						
27968 ENU11763		25-47	742-762	CDS	U34740						
27969 ENU11764		25-44	758-777	CDS	U96847						
27970 ENU11765		25-48	778-804	CDS	M19132						
27971 ENU11766		25-45	945-969	CDS	X13525						
27972 ENU11767		25-44	1002-	CDS	M16196						
			1029								
27973 ENU11768		25-44	1024-	CDS	Z49875						
			1046								
27974 ENUI1769		25-51	1031-	CDS	AF032988						
27975 FMIII 1770		25.48	1053	CDS	M22869						
		2+	1107								
27976 ENUI1771		25-46	1114-	CDS	AJ001157						
			1135								
27977 ENUI 1772		25-44	1222-	CDS	AF098669						
			1242								
27978 ENU11773		25-45	1258-	CDS	M20631						
			1278	ć							
2/9/9 ENUII7/4		25-43	1270-	CDS	AF029318						
27980 ENUI1775		25-43	1293	CDS	U19394						
		;	1293								

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Blast Prob																		
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aat Score																		
ncbi gi																		
Database Hit ncbi gi U28383	S79392	M17519	M17520	S79392	M16197	AF043230	U34740	U73194	X71807	Z83333	AF023156	Z54244	D87895	L36341	AF043332	AF036763	AF016187 AJ011295	U81827
Selection Basis CDS	CDS	CDS																
Primer 3 pos 1270-	1299 1291-	1311 1299-	1323 1305-	1329 1403-	1423 1451-	1473 1466-	1494 1473-	1500 1654-	1680 1803-	1827 2356-	2376 2367-	2394 2485-	2508 2842-	2865 2894-	2922 2931-	2952 2931-	2952 188-219 215-246	232-264
Primer 5 pos 25-47	25-44	25-48	25-48	25-44	25-48	25-43	25-52	25-45	25-57	25-49	25-44	25-47	25-50	25-45	25-46	25-46	25-51	25-51
Contig source																		
Seq num Seq id 27981 ENU11776	27982 ENU11777	27983 ENU11778	27984 ENU11779	27985 ENU11780	27986 ENU11781	27987 ENU11782	27988 ENU11783	27989 ENU11784	27990 ENU11785	27991 ENU11786	27992 ENU11787	27993 ENU11788	27994 ENUII789	27995 ENU11790	27996 ENU11791	27997 ENU11792	27998 ENU11793 27999 ENU11794	28000 ENUI1795

Seq num Seq id Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	a ncbi gi	aat Score	Blast Score	Blast Prob	% % id cvrg	% cvrg Description
ENU11796 ENU11797	25-48 25-44	267-291 266-291	CDS CDS	U12631 X55549						
ENU11798	25-45	267-291	CDS	X55550						
ENU11799 FNT111800	25-51	292-321	S C	M83141 M18258						
28006 ENU11801	25-49	380-402	CDS	U12630						
28007 ENU11802	25-47	400-426	CDS	M65259						
28008 ENU11803	25-49	483-510	CDS	AF035768						
28009 ENU11804	25-48	496-528	CDS	AJ011296						
28010 ENU11805	25-48	522-546	CDS	M82941						
ENU11806	25-47	603-627	CDS	U34740						
ENU11807	25-47	603-627	CDS	L27825						
28013 ENU11808	25-49	635-663	CDS	U35731						
28014 ENU11809	25-47	743-771	CDS	U78083						
28015 ENU11810	25-50	761-786	CDS	U28333						
28016 ENU11811	25-47	759-792	CDS	M59935						
28017 ENU11812	25-49	776-804	CDS	U34740						
28018 ENU11813	25-51	809-840	CDS	U34740						
ENU11814	25-48	840-873	CDS	U34740						
28020 ENU11815	25-52	870-891	CDS	AJ224085						
ENU11816	25-51	883-915	CDS	U34740						
ENU11817	25-49	918-942	CDS	U59215						
ENU11818	25-49	925-951	CDS	U62482						
ENU11819	25-47	926-951	CDS	M27067						
ENU11820	25-48	096-086	CDS	U05592						
28026 ENU11821	25-44	943-972	CDS	X13525						
28027 ENU11822	25-50	945-975	CDS	A10846						
ENU11823	25-46	962-990	CDS	M33539						
ENU11824	25-46	1006-	CDS	Y13768						
		1029								
28030 ENU11825	25-44	1014-	CDS	AF056182						
		1038								
28031 ENU11826	25-53	1007-	CDS	U49917						
C001111W0		1041	Ç	4.0003470						
28032 ENUI182/	25-55	1018-	SCDS	Ar083468						
		1044								

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Database Hit ncbi gi X53310	M29819	U59215	Z11612	X98065	U34740	M77665	Y13700	L31778	U83489	AF043231	D87063	L03563	M27549	U22009	M83571	U30797	X16121
Selection Basis CDS	CDS																
Primer 3 pos 1028-	1026-	1059 1056-	1080 1088-	1113 1095-	1128	1143	1176 1149-	1182	1191 1163-	1197	1218 1208-	1230 1204-	1230 1212-	1245 1280-	1314	1320 1303-	1326 1336- 1359
Primer 5 pos 25-53	25-48	25-46	25-49	25-48	25-45	25-48	25-51	25-48	25-48	25-54	25-60	25-48	25-49	25-49	25-51	25-57	25-49
Contig source																	
Seq num Seq id 28033 ENU11828	28034 ENU11829	28035 ENU11830	28036 ENU11831	28037 ENU11832	28038 ENU11833	28039 ENU11834	28040 ENU11835	28041 ENU11836	28042 ENU11837	28043 ENU11838	28044 ENU11839	28045 ENU11840	28046 ENU11841	28047 ENU11842	28048 ENU11843	28049 ENU11844	28050 ENU11845

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Blast																	
aat Score																	
ncbi gi																	
Database Hit ncbi gi X64602	X15647	U34740	U34382	Y13759	U47318	M36918	X56671	X13525	X62696	M60528	AF013590	U95045	X82541	AJ000996	M83569	X52552	AF080599
Selection Basis CDS	CDS																
Primer 3 pos 1387-	1416 1443-	1476 1455-	1482 1476-	1503 1489-	1509 1518-	1542 1531-	1560 1540-	1566 1553-	1581 1561-	1590 1614-	1647 1627-	1656 1679-	1701 1676-	1704	1752 1729-	1752 1781-	1809 1927- 1956
Primer 5 pos 25-51	25-47	25-50	25-48	25-50	25-57	25-45	25-45	25-45	25-60	25-47	25-53	25-49	25-49	25-47	25-49	25-49	25-50
Contig source		•	•	.,				.,	.,	•	.,		• • •	•••	• •	• • •	.,
Seq num Seq id 28051 ENU11846	28052 ENU11847	28053 ENU11848	28054 ENU11849	28055 ENU11850	28056 ENU11851	28057 ENU11852	28058 ENU11853	28059 ENU11854	28060 ENU11855	28061 ENU11856	28062 ENU11857	28063 ENU11858	28064 ENU11859	28065 ENU11860	28066 ENU11861	28067 ENU11862	28068 ENU11863

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Blast Prob																	
Blast																	
aat Score																	
ncbi gi																	
Database Hit ncbi gi L24395	U47540	U37803	AF043229	M31517	X64603	X99624	9699SU	J04850	Y13568	X59269	AJ223459	X06252	M24071	L27817	U56097	U91968	X52491
Selection Basis CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS
Primer 3 pos 2114-	2145 2176-	2199 2190-	2214 2197-	2226 2254-	22 <i>77</i> 2261-	2292 2283-	2307 2278-	2307	2370 2358-	2388 2373-	2400 2406-	2436 2431-	2457 2544-	2574 2550-	2577 2562-	2583 2566-	2595 2581- 2610
Primer 5 pos 25-51	25-48	25-50	25-50	25-47	25-54	25-48	25-49	25-51	25-49	25-52	25-45	25-48	25-44	25-51	25-49	25-52	25-46
Contig source																	
Seq num Seq id 28069 ENU11864	28070 ENU11865	28071 ENU11866	28072 ENU11867	28073 ENU11868	28074 ENU11869	28075 ENU11870	28076 ENU11871	28077 ENU11872	28078 ENU11873	28079 ENU11874	28080 ENU11875	28081 ENU11876	28082 ENU11877	28083 ENU11878	28084 ENU11879	28085 ENU11880	28086 ENU11881
Seq num 28069	28070	28071	28072	28073	28074	28075	28076	28077	28078	28079	28080	28081	28082	28083	28084	28085	28086

		Primer	Primer	Selection			Blast	Blast	%	
num Seq id 28087 ENU11882	Contig source	5 pos 25-51	3 pos 2593-	Basis CDS	Database Hit ncbi gi L28810	Score	Score	Prob	% id cvrg Description	
28088 ENU11883		25-48	2622 2626-	CDS	AF014813					
28089 ENU11884		25-47	2649 2634-	CDS	M68900					
28090 ENU11885		25-44	2658 2663-	CDS	M59935					
28091 ENU11886		25-44	2685 2663-	CDS	M77664					
28092 ENUI1887		25-45	2706-	CDS	D83216					
28093 ENU11888		25-45	2709-	CDS	D21269					
28094 ENU11889			2730	CDS	L03200					
28095 ENU11890				CDS	X05204					
28096 ENU11891				CDS	X65866					
28097 ENU11892				CDS	M32075					
28098 ENU11893				CDS	U86620					
28099 ENUI1894				CDS	U86619					
28100 ENU11895				CDS	M35967					
28101 ENU11896				CDS	09690X					
28102 ENU11897				CDS	101390					

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Blast Prob													
Blast													
aat Score													
ncbi gi													
Database Hit ncbi gi X72210	Z49894	X15442	V00650	X06961	U74303	U34740	U62332	06200X	U07935	X55548	M30144	X54668	M61113
Selection Basis CDS	CDS												
Primer 3 pos													
Primer 5 pos													
Contig source		-											
Seq num Seq id 28103 ENU11898	28104 ENU11899	28105 ENU11900	28106 ENU11901	28107 ENU11902	28108 ENU11903	28109 ENU11904	28110 ENU11905	28111 ENU11906	28112 ENU11907	28113 ENU11908	28114 ENU11909	28115 ENU11910	28116 ENU11911

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 28117 ENU11912	Selection Basis CDS	Database Hit ncbi gi U35341	aat Score	Blast	Blast Prob	% id cvrg	Description
28118 ENU11913	CDS	AF013602					
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28120 ENU11915	CDS	X52565					
28121 ENU11916	CDS	U03025					
28122 ENU11917	CDS	Z49893					
28123 ENU11918	CDS	M77283					
28124 ENU11919	CDS	L27825					
28125 ENU11920	CDS	U34740					
28126 ENU11921	CDS	Z50175					
28127 ENU11922	CDS	U19882					
28128 ENU11923	CDS	U18265					
28129 ENU11924	CDS	U07169					
28130 ENU11925	CDS	X02764					

## noucker company

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 28131 ENU11926	Selection Basis CDS	Database Hit ncbi gi M77665	aat Blast Blast Score Score Prob	% % id cvrg Description
28132 ENU11927	CDS	AF069492		
28133 ENU11928	CDS	Z48000		
28134 ENU11929	CDS	U19395		
28135 ENU11930	CDS	L27825		
28136 ENU11931	CDS	AF090736		
28137 ENU11932	CDS	U71603		
28138 ENU11933	CDS	M74120		
28139 ENU11934	CDS	U34740	·	
28140 ENU11935	CDS	U34740	-	
28141 ENU11936	CDS	U59803		
28142 ENU11937	CDS	U70044		
28143 ENU11938	CDS	X84001		
28144 ENU11939	CDS	U34740		

Seq Primer Primer num Seq id Contig source 5 pos 3 pos 28145 ENU11940	Selection Basis CDS	Database Hit ncbi gi X77830	aat Blast Blast Score Score Prob	% % id cvrg Description
28146 ENU11941	CDS	AF029885		
28147 ENU11942	CDS	U13919		
28148 ENU11943	CDS	7979TX		
28149 ENU11944	CDS	X64601		
28150 ENU11945	CDS	X74327		
28151 ENU11946	CDS	96797X		
28152 ENU11947	CDS	AF085679		
28153 ENU11948	CDS	AJ007629		
28154 ENU11949	CDS	X98931		
28155 ENU11950	CDS	Z79750		
28156 ENU11951	CDS	AF014812		
28157 ENU11952	CDS	X64170		
28158 ENU11953	CDS	X16990		

## nguntan napag

Seq num Seq id 28159 ENU11954	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis CDS	Database Hit ncbi gi AF070480	aat Score	Blast	Blast Prob	% % id cvrg Description	scription
28160 ENU11955				CDS	Z47081					
28161 ENU11956				CDS	AF080600					
28162 ENU11957				CDS	M20249					
28163 ENU11958				CDS	X86399					
28164 ENU11959				CDS	U80672					
28165 ENU11960	_			CDS	X02390					

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